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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:03 ; Search time 33.873 Seconds
(without alignments)
1526.325 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLLFLNVCIFICG.....PVKIKSVSMKIRRMYPYRK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID2/gcgdata/geneseq-emb1/AA1980.DAT:*
2: /SID2/gcgdata/geneseq-emb1/AA1981.DAT:*
3: /SID2/gcgdata/geneseq-emb1/AA1982.DAT:*
4: /SID2/gcgdata/geneseq-emb1/AA1983.DAT:*
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22: /SID2/gcgdata/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	388	22	Human prothrombina
2	2100	99.8	388	22	Human angiotensin
3	2086	99.1	388	23	Human polypeptide
4	2000	95.1	368	22	Human prothrombina
5	1729	82.2	326	22	Human novel protei
6	1729	82.2	326	22	Human novel protei
7	1729	82.2	326	22	Human prothrombina
8	1711.5	81.3	335	23	Human MDPF SEQ ID
9	1625	77.2	306	22	Human prothrombina
10	1299	61.7	237	22	Human prothrombina

11	1265	60.1	240	22	Human prothrombina
12	634	30.1	141	22	Novel human diagno
13	628.5	29.9	138	22	Novel human diagno
14	521	24.8	116	22	Novel human diagno
15	425	20.2	491	20	Human zapot protei
16	425	20.2	491	20	Human TIE ligand N
17	425	20.2	491	21	Angiotensin-like
18	425	20.2	491	21	Human PRO188 prote
19	425	20.2	491	21	Amino acid sequenc
20	425	20.2	491	21	An angiotensin-re
21	425	20.2	491	22	Human PRO188 polyp
22	425	20.2	491	22	Human neovasculari
23	425	20.2	491	22	Human angiotensin
24	425	20.2	491	23	Human TIE ligand N
25	421	20.0	491	21	Human secreted pro
26	420	20.0	491	21	Protein encoded by
27	414	19.7	439	20	Human polypeptide
28	413.5	19.7	439	20	Human prothrombina
29	405.5	19.3	432	20	Mouse prothrombina
30	403.5	19.2	497	17	Human TIE-2 ligand
31	403.5	19.2	497	17	Human TIE-2 ligand
32	403.5	19.2	497	19	Human TIE-2 ligand
33	401.5	19.1	360	21	Amino acid sequenc
34	400.5	19.0	493	21	Mouse angiotensin
35	400	19.0	386	20	Human ORFX ORF1476
36	400	19.0	493	20	Human normal uteru
37	400	19.0	493	21	Human TIE ligand N
38	400	19.0	493	21	Angiotensin-like
39	400	19.0	493	21	PSBO-3 protein enc
40	400	19.0	493	22	Human scarface 1 p
41	400	19.0	493	22	Human PRO196 polyp
42	400	19.0	493	22	Amino acid sequenc
43	400	19.0	493	22	Human 410 angioten
44	400	19.0	493	23	Human angiotensin
45	400	19.0	493	23	Human matrix-remod
					Human TIE ligand N

ALIGNMENTS

RESULT 1	AA82584	
ID	AA82584 standard; Protein; 388 AA.	
XX	AA82584;	
AC		
XX		
DT	02-OCT-2001 (first entry)	
XX		
DE	Human prothrombinase-like polypeptide.	
XX		
KW	Prothrombinase-like polypeptide; human; haemostatic; cardiant;	
KW	nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;	
KW	antiartherosclerotic; antitumor; vulnerrary; osteoporosis;	
KW	immunomodulatory; antirheumatic; antidiarrhetic; antiinflammatory;	
XX	thrombolytic; diagnosis; therapy.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	/label= Signal_peptide
FT		21..388
FT		/label= Mature.protein
FT	Domain	/note= "separately claimed in Claim 10"
FT		181..217
FT		/note= "fibrinogen beta/gamma chain"
FT	Domain	/note= "separately claimed in Claim 10"
FT		222..234
FT		/note= "fibrinogen beta/gamma chain"
FT		/note= "separately claimed in Claim 10"
FT	Domain	271..285
FT		/note= "fibrinogen beta/gamma chain"
FT		/note= "separately claimed in Claim 10"

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FT      Domain
FT      324..353
FT      /note="fibrinogen beta/gamma chain"
FT      /note="separately claimed in Claim 10"
XX      WO200153456-A2.
XX      26-JUL-2001.
XX      22-DEC-2000; 2000WO-US35061.
XX      21-JAN-2000; 2000US-0488725.
XX      25-JAN-2000; 2000US-0491404.
XX      25-APR-2000; 2000US-0552317.
XX      17-JUN-2000; 2000US-0596196.
XX      31-AUG-2000; 2000US-0643313.
XX      (HYSE-) HXSEQ INC.
XX      Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX      Arterburn MC, Tang YT, Liu C, Drmanac R;
XX      WPI: 2001-483140/52.
XX      DR      N-PSDB; AAH26235; AAH26236.
XX      Novel prothrombinase-like polypeptides and polynucleotides useful in
XX      diagnosing and treating e.g. myocardial infarction and diabetes -
XX      Claim 10; Page 126-127; 140pp; English.
XX      The present sequence is that of a novel human secreted
XX      prothrombinase-like polypeptide (PLP). The polypeptide has a
XX      predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid
XX      sequence similarity to human prothrombinase Fg12 protein. The
XX      sequence was predicted from polynucleotides (see AAH26235-36)
XX      derived from a human ovary cDNA clone. PLP polynucleotides and
XX      polypeptides, including the mature protein, polypeptides including
XX      PLP fibrinogen chains, and a soluble splice variant (see AAH82590),
XX      can be used in the diagnosis, treatment and/or prevention of diseases
XX      associated with the dysregulation of coagulation pathways, such as
XX      haemophilia, myocardial infarction, glomerular disease, diabetes,
XX      fulminant viral hepatitis and atherosclerosis. They may also be
XX      beneficial in the treatment of viral infections and some forms of
XX      cancer. A claimed method of treating a subject in need of enhanced
XX      PLP activity or expression involves the administration of PLP, a
XX      PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX      treating a subject having need to inhibit activity or expression of
XX      PLP involves the administration of a PLP antagonist, a
XX      polynucleotide that inhibits expression of a PLP polynucleotide,
XX      or a polypeptide that competes with the PLP for its ligand. The
XX      polypeptides can also be used to raise antibodies, as food
XX      supplements, and to screen for agonists and antagonists.
XX      SO      Sequence 388 AA:
XX      Query Match 100.0%; Score 2104; DB 22; Length 388;
XX      Best Local Similarity 100.0%; Pred. No. 8 6e-205;
XX      Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 MMSPSQASLLFLNVCIFTCGEVVGNCVHSTDSVYNIVEDGSSNAKDESKNDYCKED 60
XX      1 MMSPSQASLLFLNVCIFTCGEVVGNCVHSTDSVYNIVEDGSSNAKDESKNDYCKED 60
XX      1 MMSPSQASLLFLNVCIFTCGEVVGNCVHSTDSVYNIVEDGSSNAKDESKNDYCKED 60
XX      61 CEESCDVTKTKTRREKHEKRCMLONSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIM 120
XX      61 CEESCDVTKTKTRREKHEKRCMLONSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIM 120
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XX      121 NVVLLTTEVERFKQDPPPHRPVOSHGLDCTPIKDTIGSVTKTPSGLYTIHHEGSSYPE 180
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XX      181 VMCDDYRGCGWTVLQKRIDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFYIVQKNKS 240
XX      181 VMCDDYRGCGWTVLQKRIDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFYIVQKNKS 240
XX      181 VMCDDYRGCGWTVLQKRIDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFYIVQKNKS 240

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QY      241 FMYLYALSEDDTLIAYSYDNFMLEDETRFPMHIGRYSNGNADAFRGTKKEDNONAMPF 300
QY      241 FMYLYALSEDDTLIAYSYDNFMLEDETRFPMHIGRYSNGNADAFRGTKKEDNONAMPF 300
DB      301 STSDVDNDGCRPACIYNGSVKSCSHLHNTGWMFNECGIAMLNIGIHFSGLATGIOM 360
DB      301 STSDVDNDGCRPACIYNGSVKSCSHLHNTGWMFNECGIAMLNIGIHFSGLATGIOM 360
QY      361 GTWTKNNSPVKTIKSVSMKTRRMNPFYK 388
QY      361 GTWTKNNSPVKTIKSVSMKTRRMNPFYK 388
DB      361 GTWTKNNSPVKTIKSVSMKTRRMNPFYK 388
RESULT 2
AAV72622
ID      AAV72622 standard; Protein; 388 AA.
XX      AC      AAV72622;
XX      DT      02-MAY-2001 (first entry)
XX      DE      Human angiotensin protein, CG144.
XX      KW      Human: angiotensin; angiotensin; gene therapy; CG144;
XX      KW      vascular stability; neovascularisation; nutritional supplement; therapy;
XX      KW      myocardial infarction; proliferative retinopathy; atherosclerosis;
XX      KW      coronary heart disease; arterial ischaemia; bone disorder; cancer;
XX      KW      abnormal vascular growth; anaemia; chronic inflammation; immune disorder;
XX      KW      haematopoiesis related disorder; coagulation disorder; leukaemia;
XX      KW      cytostatic; vasotropic; food supplement; nervous system disorder;
XX      KW      drug screening.
XX      OS      Homo sapiens.
XX      FH      Key Location/Qualifiers
XX      FT      Peptide 1..22
XX      FT      /label= Signal-peptide
XX      FT      Protein 23..388
XX      FT      /note= "Mature angiotensin protein, CG144"
XX      FT      Domain 193..230
XX      FT      /note= "Fibrinogen domain"
XX      FT      Domain 234..247
XX      FT      /note= "Fibrinogen domain"
XX      FT      Domain 283..301
XX      FT      /note= "Fibrinogen domain"
XX      FT      Domain 307..321
XX      FT      /note= "Fibrinogen domain"
XX      FT      Domain 337..366
XX      FT      /note= "Fibrinogen domain"
XX      PN      WO200105825-A2.
XX      PD      25-JAN-2001.
XX      PF      17-JUL-2000; 2000WO-US19429.
XX      PR      16-JUL-1999; 99US-0354881.
XX      PA      (HYSE-) HXSEQ INC.
XX      PI      Ballinger DG, Montgomery JR;
XX      DR      WPI: 2001-091966/10.
XX      DR      N-PSDB; AAD02607.
XX      PT      Human angiotensin proteins and DNA encoding sequences useful for
XX      PT      preventing, treating or ameliorating a medical condition in a mammalian
XX      PT      subject e.g. arthritis and cancer -
XX      PS      Claim 10; Page 111-112; 132pp; English.
XX      CC      The present sequence is human angiotensin protein, CG144.

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CC The present invention relates to human angiotensin polypeptides such
 CC as CG006, CG007, CG015, CG144 and CG250. The angiotensin polypeptides
 CC are used as hybridisation probes, for chromosome and gene mapping, to
 CC identify polymorphism and for recombinant protein production.
 CC Angiotensin may be useful for modulating vascular stability and
 CC neovascularisation associated with various pathologies. It is used as a
 CC nutritional supplement, molecular weight marker and in gene therapy. It
 CC is also used for preventing, treating or ameliorating angiogenesis
 CC related disorders such as myocardial infarction, proliferative
 CC retinopathy, atherosclerosis, coronary heart disease, arterial
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,
 CC anaemia and chronic inflammatory reactions (e.g., asthma and arthritis) and immune
 CC disorders (e.g., inflammatory reactions and autoimmune diseases),
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell
 CC deficiencies), coagulation disorders, leukaemias and nervous system
 CC disorders. It is also used in drug screening techniques for screening
 CC compounds which are able to modulate the expression or activity of
 CC angiotensin. The compounds can also be used to treat diseases and
 CC disorders.

XX Sequence 388 AA;

Query Match 99.8%; Score 2100; DB 22; Length 388;

Best Local Similarity 99.7%; Pred. No. 2.2e-204; Mismatches 1; Indels 0; Gaps 0;

Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMSPSQASLFLNVCIFGCEVGNVCYHSTDSVNIIVEDGSNAKDESKNDTVCKED 60
 DB 1 MMSPSQASLFLNVCIFGCEVGNVCYHSTDSVNIIVEDGSNAKDESKNDTVCKED 60

QY 61 CEESCDVTKITREKHEKRCNLQNSIVSYSTRSKLLRNMMDEQASLDYLSQVNELM 120
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QY 121 NRVLTLTEVFRKQDPPRHPVOSHGLDCTDIDKDTISVTKPSGLYIIHPEGSSYFE 180
 DB 121 NRVLTLTEVFRKQDPPRHPVOSHGLDCTDIDKDTISVTKPSGLYIIHPEGSSYFE 180

QY 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEWGLKRIFYIYQNKMTS 240
 DB 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEWGLKRIFYIYQNKMTS 240

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 DB 241 FMLVYALSEDDTLAYASYDNFWLEDETRFPMHIGRYSNGADAFRLKKEDNONAMPF 300

QY 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLLATGIGIOW 360
 DB 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLLATGIGIOW 360

QY 361 GTWTKNNSPVKIKSVSMKIRRMYPYFK 388
 DB 361 GTWTKNNSPVKIKSVSMKIRRMYPYFK 388

RESULT 3
 ABB77546
 ID ABB77546 standard; Protein; 388 AA.

XX ABB77546;

XX 05-AUG-2002 (first entry)

XX Human polypeptide SEQ ID NO 2.

XX Human; collagen II; aggrecan; antiarthritic; cartilage;

XX arthritis deformans.

XX Homo sapiens.

XX MO200242448-A1.
 XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-JP10150.
 XX
 XX 22-NOV-2000; 2000JP-0356378.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 XX Yasunaga K;
 XX
 XX WPI: 2002-463631/49.
 XX N-PSDB: ABL60374.

XX Human polypeptide promoting collagen II and aggrecan production for
 XX treatment and prevention of arthritis deformans -
 XX
 XX Claim 1; Page 56-57; 72pp; Japanese.

XX The invention relates to human polypeptide (ABB77546) promoting collagen
 XX II and/or aggrecan activity created by addition, deletion and/or
 XX substitution. The polypeptide has antiarthritic activity and promotes
 XX collagen II and aggrecan production in cartilage cells. It is useful for
 XX treatment and prevention of arthritis deformans.

XX Sequence 388 AA;

Query Match 99.1%; Score 2086; DB 23; Length 388;

Best Local Similarity 99.5%; Pred. No. 5.8e-203; Mismatches 2; Indels 0; Gaps 0;

Matches 386; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 61 CEESCDVTKITREKHEKRCNLQNSIVSYSTRSKLLRNMMDEQASLDYLSQVNELM 120

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 DB 121 NRVLTLTEVFRKQDPPRHPVOSHGLDCTDIDKDTISVTKPSGLYIIHPEGSSYFE 180

QY 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEWGLKRIFYIYQNKMTS 240
 DB 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEWGLKRIFYIYQNKMTS 240

QY 241 FMLVYALSEDDTLAYASYDNFWLEDETRFPMHIGRYSNGADAFRLKKEDNONAMPF 300
 DB 241 FMLVYALSEDDTLAYASYDNFWLEDETRFPMHIGRYSNGADAFRLKKEDNONAMPF 300

QY 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLLATGIGIOW 360
 DB 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLLATGIGIOW 360

QY 361 GTWTKNNSPVKIKSVSMKIRRMYPYFK 388
 DB 361 GTWTKNNSPVKIKSVSMKIRRMYPYFK 388

RESULT 4
 AAB82589
 ID AAB82589 standard; Protein; 368 AA.

XX AAB82589;

XX 02-OCT-2001 (first entry)

XX Human prothrombinase-like polypeptide (mature protein).

XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;

XX nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;
 XX antiatherosclerotic; antileukemic; vulnary; osteoporosis;
 XX immunomodulatory; antineumatic; antiarthritic; antiinflammatory;
 XX thrombolytic; diagnosis; therapy.

```

XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 161..197
XX /note= "fibrinogen beta/gamma chain"
XX Domain 202..214
XX /note= "fibrinogen beta/gamma chain"
XX Domain 251..265
XX /note= "fibrinogen beta/gamma chain"
XX Domain 304..333
XX /note= "fibrinogen beta/gamma chain"
XX
XX WO200153456-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35061.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-JAN-2000; 2000US-0491404.
XX 25-APR-2000; 2000US-0552317.
XX 17-JUN-2000; 2000US-0596196.
XX 31-AUG-2000; 2000US-0643313.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
XX N-PSDB: AAH26235, AAH26236.
XX
XX Novel prothrombinase-like polypeptides and polynucleotides useful in
XX diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX Claim 10; Page 128-129; 140pp; English.
XX
XX The present sequence is that of human secreted prothrombinase-like
XX polypeptide (PLP) mature polypeptide, as predicted from
XX polynucleotides (see AAH26235-36) derived from an ovary cDNA clone.
XX PLP polynucleotides and polypeptides, including the mature protein,
XX can be used in the diagnosis, treatment and/or prevention of diseases
XX associated with the dysregulation of coagulation pathways, such as
XX haemophilia, myocardial infarction, glomerular disease, diabetes,
XX fulminant viral hepatitis and atherosclerosis. They may also be
XX beneficial in the treatment of viral infections and some forms of
XX cancer. A claimed method of treating a subject in need of enhanced
XX PLP activity or expression involves the administration of PLP, a
XX PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX treating a subject having need to inhibit activity or expression of
XX PLP involves the administration of a PLP antagonist, a
XX polynucleotide that inhibits expression of a PLP polynucleotide,
XX or a polypeptide that competes with the PLP for its ligand. The
XX polypeptides can also be used to raise antibodies, as food
XX supplements, and to screen for agonists and antagonists.
XX
XX Sequence 368 AA:
XX
XX Query Match 95.1%; Score 2000; DB 22; Length 368;
XX Best Local Similarity 100.0%; Pred. No. 2,9e-194;
XX Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 21 EVVQNCVHNSHSDSSVNVIVEDGSSNAKDESKNDYVCKDESCDVTKRTIREKHFMK 80
XX 1 EVVQNCVHNSHSDSSVNVIVEDGSSNAKDESKNDYVCKDESCDVTKRTIREKHFMK 60
XX
XX 81 RMLQNSIVSYTSTKTKLLNNMDEQOASLDYLSNOVNEMLNRYLLTTFVFRKQDLPFP 140
XX 61 RMLQNSIVSYTSTKTKLLNNMDEQOASLDYLSNOVNEMLNRYLLTTFVFRKQDLPFP 120
XX
XX 141 RVQSHGLDCTDIKDTIGSVTKTPSGLYTIHPGSSYPEFVCMQMDYRGGGWTVIQKRID 200
XX

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DB 121 RVQSHGLDCTDIKDTIGSVTKTPSGLYTIHPGSSYPEFVCMQMDYRGGGWTVIQKRID 180
QY 201 GIIDFQRLMCDYLDGFGDLLGEFMIGLKKIEFYIVNOKNTSFMULYVALESEBDPTLAAASYD 260
DB 181 GIIDFQRLMCDYLDGFGDLLGEFMIGLKKIEFYIVNOKNTSFMULYVALESEBDPTLAAASYD 240
QY 261 NFWLEDETREFKMHILGRYSNAGDARGLKKEPNQANAFSTSDVNDGCRPACLVNGOS 320
DB 241 NFWLEDETREFKMHILGRYSNAGDARGLKKEPNQANAFSTSDVNDGCRPACLVNGOS 300
QY 321 VKSCSHLHNKTGMWFNDEGLANLNGIHFHSGKLLATGIOMGTWKNNSPVKIKSVSMKIR 380
DB 301 VKSCSHLHNKTGMWFNDEGLANLNGIHFHSGKLLATGIOMGTWKNNSPVKIKSVSMKIR 360
QY 381 RMYNPFYK 388
DB 361 RMYNPFYK 368
XX
XX RESULT 5
XX AAU14275
XX ID AAU14275 standard; Protein; 326 AA.
XX
XX AAU14275;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human novel protein #146.
XX
XX Human: novel protein; cytostatic; osteoprotic; antiinflammatory;
XX immunomodulatory; cytoskeletal; neuroprotective; vulnerrary; nocitopic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.
XX
XX Homo sapiens.
XX
XX WO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-451939/48.
XX N-PSDB: AAS22580.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 605; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX polypeptides. Polynucleotides of the invention are used as probes and
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicits an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.
XX

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CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

XX
 SO Sequence 326 AA:

Query Match 82.2%; Score 1729; DB 22; Length 326;
 Best Local Similarity 84.0%; Pred. No. 8.4e-167;
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 DB 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 QY 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRNMDEQOASLDYLSNOVVELM 120
 DB 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRNMDEQOASLDYLSNOVVELM 120
 QY 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 DB 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 QY 181 VMCDMDYRGGMWYIQRIGIIDFORLWCDYLDGFEDLLGEFMLGLKAFIYVQKNTS 240
 DB 181 VMCDMDYRGGMWYIQRIGIIDFORLWCDYLDGFEDLLGEFMLGLKAFIYVQKNTS 240
 QY 241 FMLVVALESEDDTLAVASYDNFMLEDETRFCKMHLGRYSNAGDAFGLKKEQNONAMP 300
 DB 221 -----GDAFGLKKEQNONAMP 300
 QY 301 STSDVDNDGCRPACLVNGQSVKCSHLHNKTMWFMNCGLANLNGIHFFSGKLATGIOW 360
 DB 239 STSDVDNDGCRPACLVNGQSVKCSHLHNKTMWFMNCGLANLNGIHFFSGKLATGIOW 298
 QY 361 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 388
 DB 299 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 326

RESULT 6

AA014511 standard; Protein; 326 AA.

AA014511:

24-OCT-2001 (first entry)

Human novel protein #382.

Human: novel protein; Antianaemic; osteopathic; antiinflammatory;
 immunomodulatory; cytosolic; neuroprotective; vulnerrary; nocotropic;
 anticonvulsant; antiallergic; ceroidprotective; antifungal; antiviral;
 antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
 chondrolytic; immunogen; antibody; gene therapy; neurological disorder;
 Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

PR 25-JAN-2000; 2000US-0491404.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-451939/48.
 DR N-PSDB; AAS22816.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 PS Example 4; Page 848-849; 894pp; English.

XX The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicits an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

SO Sequence 326 AA:

Query Match 82.2%; Score 1729; DB 22; Length 326;
 Best Local Similarity 84.0%; Pred. No. 8.4e-167;
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 DB 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 QY 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRNMDEQOASLDYLSNOVVELM 120
 DB 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRNMDEQOASLDYLSNOVVELM 120
 QY 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 DB 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 QY 181 VMCDMDYRGGMWYIQRIGIIDFORLWCDYLDGFEDLLGEFMLGLKAFIYVQKNTS 240
 DB 181 VMCDMDYRGGMWYIQRIGIIDFORLWCDYLDGFEDLLGEFMLGLKAFIYVQKNTS 240
 QY 241 FMLVVALESEDDTLAVASYDNFMLEDETRFCKMHLGRYSNAGDAFGLKKEQNONAMP 300
 DB 221 -----GDAFGLKKEQNONAMP 300
 QY 301 STSDVDNDGCRPACLVNGQSVKCSHLHNKTMWFMNCGLANLNGIHFFSGKLATGIOW 360
 DB 239 STSDVDNDGCRPACLVNGQSVKCSHLHNKTMWFMNCGLANLNGIHFFSGKLATGIOW 298
 QY 361 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 388
 DB 299 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 326

PR 06-SEP-2000; 2000US-230514P.
 PR 06-SEP-2000; 2000US-230515P.
 PR 06-SEP-2000; 2000US-230517P.
 PR 06-SEP-2000; 2000US-230518P.
 PR 06-SEP-2000; 2000US-230519P.
 PR 06-SEP-2000; 2000US-230595P.
 PR 06-SEP-2000; 2000US-230597P.
 PR 06-SEP-2000; 2000US-230598P.
 PR 06-SEP-2000; 2000US-230599P.
 PR 06-SEP-2000; 2000US-230610P.
 PR 06-SEP-2000; 2000US-230865P.
 PR 06-SEP-2000; 2000US-230988P.
 PR 06-SEP-2000; 2000US-230989P.
 PR 07-SEP-2000; 2000US-230951P.
 PR 07-SEP-2000; 2000US-231163P.
 PR 07-SEP-2000; 2000US-231167P.
 XX (INCYTE GENOMICS INC.)
 PA Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR,
 PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM,
 PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A,
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Iman RR,
 XX WPI: 2002-527544/56.
 DR N-PSDB; ABQ72639.

PT Novel human disease detection and treatment polypeptide, useful in
 PT diagnosis, prevention or treatment of cell proliferative disorders e.g.
 PT arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
 PT e.g. AIDS
 PS Claim 14; Page 576-577; 618pp; English.

XX The invention relates to an isolated human disease detection and
 CC treatment (MDPT) polypeptide (I) selected from a polypeptide having a
 CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the
 CC specification, a naturally occurring polypeptide comprising a sequence
 CC having at least 90% identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I), and for
 CC preparing a polyclonal or monoclonal antibody by hybridoma technology.
 CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
 CC screening a compound for effectiveness in altering expression of a target
 CC polynucleotide comprising oligonucleotides and antibodies are useful for
 CC detecting MDPT in a sample or for assessing toxicity of a test compound,
 CC in a diagnostic test for a condition or a disease associated with the
 CC expression of MDPT in a biological sample, for detecting (I) in a sample,
 CC and for purifying (I) from a sample. A composition comprising (I), an
 CC agonist or antagonist is useful for treating a disease or condition
 CC associated with decreased or increased expression of functional MDPT.
 CC (I) or (II) are useful for diagnosing, treating or preventing disorders
 CC associated with aberrant expression of MDPT, where the disorders are
 CC selected from a cell proliferative disorder such as arteriosclerosis,
 CC cirrhosis, hepatitis, psoriasis, and cancer and an
 CC autoimmune/inflammatory disorder such as AIDS, Addison's disease,
 CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
 CC rheumatoid arthritis. (II) are useful for creating knockin humanised
 CC animals or transgenic animals to model human diseases, in somatic or
 CC germ-line gene therapy, to generate a transcript image of a tissue or cell
 CC type, for detecting differences in the chromosomal location due to
 CC translocation or inversion among normal, carrier or affected individuals
 CC and as hybridisation probes for mapping naturally occurring genomic
 CC sequences.

SQ Sequence 335 AA;
 Query Match 81.3%; Score 1711.5; DB 23; Length 335;
 Best Local Similarity 83.0%; Pred. No. 5,3e-165;
 Matches 322; Conservative 0; Mismatches 1; Indels 65; Gaps 1;

QY 1 MASPQASLFLNLCIFCGEVQNCVHSTDSVYNIIVEDGSNADESKNDPVCKED 60
 Db 13 MASPQASLFLNLCIFCGEAVQNCVHSTDSVYNIIVEDGSNADESKNDPVCKED 72
 QY 61 CEESCDVYKTRREKHEKHCNLRNSIVSYRSTKILRNAMDDQASLDVLSNOVELM 120
 Db 73 CEESCDVYKTRREKHEKHCNLRNSIVSYRSTKILRNAMDDQASLDVLSNQ----- 127
 QY 121 NRVLLLTTEVERKQIDPEPHRPVOSHGDCTDIDITIGSVYKTPSGYIIHPESSYPFE 180
 Db 128 ----- 127
 QY 181 VMCDMDYRGCGWYIYQKRIDGIIIDFQRLMCDYLDGFGDLGEFNLGKRIYVNOKNTS 240
 Db 128 VMCDMDYRGCGWYIYQKRIDGIIIDFQRLMCDYLDGFGDLGEFNLGKRIYVNOKNTS 187
 QY 241 FMLVVALESEDDTLAVSYDNFMLEDEFRFKMLGRYSNAGAFRGKREDNONMPE 300
 Db 188 FMLVVALESEDDTLAVSYDNFMLEDEFRFKMLGRYSNAGAFRGKREDNONMPE 247
 QY 301 STSDVDNDGCRPACLVNGSVKSCSHLNKTGMFNECGLANLNGIHHSGLATGIGW 360
 Db 248 STSDVDNDGCRPACLVNGSVKSCSHLNKTGMFNECGLANLNGIHHSGLATGIGW 307
 QY 361 GTWTRKNSPVKIKSVSMKIRRYNPEYK 388
 Db 308 GTWTRKNSPVKIKSVSMKIRRYNPEYK 335

RESULT 9
 AAB82593
 ID AAB82593 standard; Protein; 306 AA.
 AC AAB82593;
 XX 02-OCM-2001 (first entry)
 DT Human prothrombinase-like polypeptide splice variant mature protein.

XX Prothrombinase-like polypeptide: human; haemostatic; cardiac;
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cyostatic;
 KW antidiabetic; antileukemic; anticancer; vulnery; osteoporosis;
 KW immunomodulatory; antineumatic; antithrombotic; antineoplastic;
 XX Homosapiens.
 OS Homo sapiens.
 XX W0200153456-A2.
 XX 26-JUL-2001.
 PD 22-DEC-2000; 2000WO-US35061.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-0552317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 XX (HYSE-) HYSED INC.
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 PI Arterburn MC, Tang YR, Liu C, Drmanac R;
 DR WPI: 2001-483140/52.
 DR N-PSDB; AAH26237.
 PT Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 PS Claim 10; Page 135-136; 140pp; English.
 CC The present sequence is that of the mature portion of a novel

CC secreted, soluble splice variant (see AAB82590) of novel human
CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and
CC polypeptides, including those comprising the mature protein of the
CC PLP splice variant, can be used in the diagnosis, treatment and/or
CC prevention of diseases associated with the dysregulation of
CC coagulation pathways, such as haemophilia, myocardial infarction,
CC glomerular disease, diabetes, fulminant viral hepatitis and
CC atherosclerosis. They may also be beneficial in the treatment of
CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PLP activity or expression
CC involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.

XX Sequence 306 AA:

Query Match 77.2%; Score 1625; DB 22; Length 306;
Best Local Similarity 83.2%; Pred. No. 2.8e-156;
Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

OY 21 EYVQGCYVHSDSSVYVNVEDGSNAKDESKSMDTYCKEDCESCDVTKRTTKEKHFMK 80
DB 1 EYVQGCYVHSDSSVYVNVEDGSNAKDESKSMDTYCKEDCESCDVTKRTTKEKHFMK 60
OY 81 RNLQNSIVYTRSTKKLLRNMDQOASLDYLSNOYNEIMNRVLLTTEVFRKQDLPFPH 140
DB 61 RNLQNSIVYTRSTKKLLRNMDQOASLDYLSNOYNEIMNRVLLTTEVFRKQDLPFPH 120
OY 141 RPYQSHGLDCTDVKOTIGSVYTPSGLYIHPGSSYPPEVMDMDYRGSGWTVIQKRD 200
DB 121 RPYQSHGLDCTDVKOTIGSVYTPSGLYIHPGSSYPPEVMDMDYRGSGWTVIQKRD 180
OY 201 GIIDPRLMCDYLDGFRGDLGFEWLGKKIFYYVNOKNKNSFMYVALESDDTLAASD 260
DB 181 GIIDPRLMCDYLDGFRGDLGFEWLGKKIFYYVNOKNKNSFMYVALESDDTLAASD 200
OY 261 NFWLEDETRFFKMLHGRYSGNAGDAFRGLKKEDNONAMPSTSDVNDGCRPACLVNGOS 320
DB 201 -----GDAFRGLKKEDNONAMPSTSDVNDGCRPACLVNGOS 238
OY 321 VNSGSHLANKTGWNEGCLANLNGIHFSGKLLATGIGWGTWTKNNSPVKIKSVSMKIR 380
DB 239 VNSGSHLANKTGWNEGCLANLNGIHFSGKLLATGIGWGTWTKNNSPVKIKSVSMKIR 298
OY 381 RMYNPYEK 388
DB 299 RMYNPYEK 306

RESULT 10
AAB82582
ID AAB82582 standard; Protein; 237 AA.

XX AAB82582;
XX
XX
XX 02-OCT-2001 (first entry)
XX
XX Human prothrombinase-like polypeptide C-terminal region.
XX
XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;
XX neoplastic; antidiabetic; hepatobiliary; antiviral; cytostatic;
XX antileukemic; antitumor; antineoplastic; antineoplastic;
XX immunomodulatory; antineoplastic; antineoplastic; antineoplastic;
XX thrombolytic; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers

FT Misc-difference 236 /note= "encoded by TTT"
FT Misc-difference 237 /note= "encoded by AAA"
XX
XX MO200153456-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35061.
XX
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-JAN-2000; 2000US-0491404.
XX 25-APR-2000; 2000US-0552317.
XX 17-JUN-2000; 2000US-0596196.
XX 31-AUG-2000; 2000US-0643313.
XX
XX (HYSE-) HYSEQ INC.

XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX Arterburn MC, Tang YT, Liu C, Drmanac R;
XX WPI; 2001-483140/52.
XX N-PSDB; AAB82583.
XX
XX Novel prothrombinase-like polypeptides and polynucleotides useful in
XX diagnosing and treating e.g. myocardial infarction and diabetes -
XX Example 2; Page 108; 140pp; English.

XX The present sequence is that of the predicted protein translation
XX product of a nucleic acid (see AAB82583) of the invention. It was
XX deduced using software that selects a polypeptide based on a
XX comparison of translated novel polynucleotides to known polypeptides.
XX The sequence shows 38.46% identity to human fibrinogen-like
XX protein, and corresponds to the C-terminal portion of a novel
XX prothrombinase-like polypeptide (PLP, see AAB82583). PLPs can be
XX associated with the dysregulation of coagulation pathways, such as
XX haemophilia, myocardial infarction, glomerular disease, diabetes,
XX fulminant viral hepatitis and atherosclerosis. They may also be
XX beneficial in the treatment of viral infections and some forms of
XX cancer. A claimed method of treating a subject in need of enhanced
XX PLP activity or expression involves the administration of PLP, a
XX PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX treating a subject having need to inhibit activity or expression of
XX PLP involves the administration of a PLP antagonist, a
XX polynucleotide that inhibits expression of a PLP polynucleotide,
XX or a polypeptide that competes with the PLP for its ligand.

XX Sequence 237 AA:
XX
XX Query Match 61.7%; Score 1299; DB 22; Length 237;
XX Best Local Similarity 99.6%; Pred. No. 2.5e-123;
XX Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 152 DIKDTIGSVYTPSGLYIHPGSSYPPEVMDMDYRGSGWTVIQKRDGIIDPRLMCD 211
DB 1 DIKDTIGSVYTPSGLYIHPGSSYPPEVMDMDYRGSGWTVIQKRDGIIDPRLMCD 60
OY 212 YLDGFGDLGFEWLGKKIFYYVNOKNKNSFMYVALESDDTLAASYNFMLEDETRFF 271
DB 61 YLDGFGDLGFEWLGKKIFYYVNOKNKNSFMYVALESDDTLAASYNFMLEDETRFF 120
OY 272 KMLHGRYSNAGDAFRGLKKEDNONAMPSTSDVNDGCRPACLVNGOSVKSCHLANKT 331
DB 121 KMLHGRYSNAGDAFRGLKKEDNONAMPSTSDVNDGCRPACLVNGOSVKSCHLANKT 180
OY 332 GWMFNEGCLANLNGIHFSGKLLATGIGWGTWTKNNSPVKIKSVSMKIRMYNPY 386
DB 181 GWMFNEGCLANLNGIHFSGKLLATGIGWGTWTKNNSPVKIKSVSMKIRMYNPY 235

RESULT 11
AAB82592
ID AAB82592 standard; Protein; 240 AA.
XX
AC AAB82592;
XX
DT 02-OCT-2001 (first entry)
DE Human prothrombinase-like polypeptide splice variant domain.
XX
KM Prothrombinase-like polypeptide; human; haemostatic; cardiac;
KM nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;
KM antidiabetic; antitumor; antineurotic; osteoporosis;
KM immunomodulatory; antineurotic; antidiabetic; antineurotic;
KM thrombolytic; diagnosis; therapy; blood coagulation.
XX
OS Homo sapiens.
XX
PN WO200153456-A2.
PD 26-JUL-2001.
PF 22-DEC-2000; 2000MO-US35061.
PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-0552317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
PI Haley DA, Boyle BU, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Atterburn MC, Tang YT, Liu C, Drmanac R;
XX
DR N-PSDB; AAB26237.
XX
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS Claim 10; Page 134-135; 140pp; English.
XX
XX The present sequence is that of the blood coagulation domain of a
CC secreted, soluble splice variant (see AAB82590) of novel human
CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and
CC polypeptides, including those comprising the present domain of the
CC PLP splice variant, can be used in the diagnosis, treatment and/or
CC prevention of diseases associated with the dysregulation of
CC coagulation pathways, such as haemophilia, myocardial infarction,
CC glomerular disease, diabetes, fulminant viral hepatitis and
CC atherosclerosis. They may also be beneficial in the treatment of
CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PLP activity or expression
CC involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.
XX
SQ Sequence 240 AA;
XX
Query Match 60.18; Score 1265; DB 22; Length 240;
Best Local Similarity 79.36; Pred. No. 7,4e-120;
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
OY 82 NLAQSIYSTRSTKRLRNMMDEQASLDYLSNOVNLNRRVLLTTEVFRKOLDPFHR 141
DB 1 NLAQSIYSTRSTKRLRNMMDEQASLDYLSNOVNLNRRVLLTTEVFRKOLDPFHR 60

OY 142 PVQSHGLDCTDIKDTISVTKTPSGLYIHPDGSSYPEVNCMDYRGCGMTYIQKRIDG 201
DB 61 PVQSHGLDCTDIKDTISVTKTPSGLYIHPDGSSYPEVNCMDYRGCGMTYIQKRIDG 120
OY 202 IIDFORLWCDYLDGDFGLGFWLGLKRIYIVQKNTSFLLYALSEDDTLAYASDN 261
DB 121 IIDFORLWCDYLDGDFGLGFWLGLKRIYIVQKNTSFLLYALSEDDTLAYASDN 139
OY 262 FWLEDETRFEKMLGRYSNAGDAFRLGLKEDNPNAPFSTSDVNDGCRACLVNGOSV 321
DB 140 -----GDAPFRGLKEDNPNAPFSTSDVNDGCRACLVNGOSV 178
OY 322 KCSCHLNKGTGWMFNEGLANLNGIHFGSKLALTATGQGTWTKNNSPVKIKRYSKIR 381
DB 179 KCSCHLNKGTGWMFNEGLANLNGIHFGSKLALTATGQGTWTKNNSPVKIKRYSKIR 238
OY 382 MY 383
DB 239 MY 240
RESULT 12
AABG22365
ID AABG22365 standard; Protein; 141 AA.
XX
AC AABG22365;
XX
DT 18-FEB-2002 (first entry)
DE Novel human diagnostic protein #22365.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
PD 11-OCT-2001.
PF 30-MAR-2001; 2001MO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX
DR N-PSDB; AAS86552.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52724; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 141 AA:
Query Match 30.1%; Score 634; DB 22; Length 141;
Best Local Similarity 64.3%; Pred. No. 4.3e-56;
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;
QY 178 PEVVCMDYRGSGWTVYQKRIIDFQRLMCDYLDGSGDLGERWLGKRIFFYVNVK 237
DB 9 PEVVCMDYRGSGWTVYQKRIIDFQRLMCDYLDGSGDL----- 51
QY 238 NTFMFLVLAESDDTLAVASYDNFMLEDETRFFKMHLGRYSGNAGDAPRGLKKEDNNA 297
DB 52 -----GDAFLFLKKEDNNA 66
QY 298 MFSTSDVDNDGCRPACLYNGSVKSCSHLHNTGWMFNECGLANLNGIHPSGKLLATG 357
DB 67 MFSTSDVDNDGCRPACLYNGSVKSCSHLHNTGWMFNECGLANLNGIHPSGKLLATG 126
QY 358 IQWGT 362
DB 127 IQWGT 131
RESULT 13
ABG22361
ID ABG22361 standard; Protein: 138 AA.
XX
AC ABG22361;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22352.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86548.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 52720; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA:
Query Match 29.9%; Score 628.5; DB 22; Length 138;
Best Local Similarity 64.6%; Pred. No. 1.5e-55;
Matches 126; Conservative 1; Mismatches 3; Indels 65; Gaps 1;
QY 1 MMSPGASLFLNVCIFTCGEVYVQGCYVHSDSSVNVIVEDGSKNAKDESKNDYCKED 60
DB 9 MMSPLALLFLNVCIFTCGEVYVQGCYVHSDSSVNVIVEDGSKNAKDESKNDYCKED 68
QY 61 CESCDVKTITREKHEKRNLDNSIVYSTRTKLLRNMDDEQOASLDYSNOVNELM 120
DB 69 CESCDVKTITREKHEKRNLDNSIVYSTRTKLLRNMDDEQOASLDYSNO----- 123
QY 121 NRVLLITTEVFRKQDPEFHPVQSHGLDCTDIKDTIGSVTKPSGLYIIPHEGSSYPE 180
DB 124 ----- 123
QY 181 VMCDMDYRGSGWTVI 195
DB 124 VMCDMDYRGSGWTVI 138
RESULT 14
ABG22364
ID ABG22364 standard; Protein: 116 AA.
XX
AC ABG22364;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86551.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID NO 52723; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 116 AA;
Query Match 24.8%; Score 521; DB 22; Length 116;
Best Local Similarity 93.1%; Pred. No. 9.6e-45;
Matches 95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 161 TKRTSGLYIIHPESSYFPEVCMQMDYRGSGWTYQKRIDIIIDFORLMCIYDGFGL 220
DB 13 TKRTSGLYIIHPESSYFPEVCMQMDYRGSGWTYQKRIDIIIDFORLMCIYDGFGL 72
QY 221 GEFWLGKRIYIVNOKNTSFMVVALESEDDTLAVASYDNF 262
DB 73 GEFWLGKRIYIVNOKNTSFMVVALESEDDTLAVASYDNF 114
RESULT 15
AAV26196
ID AAV26196 standard; Protein: 491 AA.
XX
AC AAV26196;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human zapo3 protein.
XX
KW Human zapo3 protein; angiotensin-1, angiotensin-2; covalently linked;
KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;
KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiotensin;
KW haematopoietic; mitogenic activity; angiogenesis; inhibitor;
KW endocrine-vascular cell association; revascularisation; DNA probe;
KW neuronal degeneration; anti-zapo3 antibody.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Peptide 1..21
FT /label= Secretory_Signal_Sequence
FT Peptide 43..48
FT /label= Immunogen
FT /note= "For production of antibodies"
FT Peptide 93..98
FT /label= Immunogen
FT /note= "For production of antibodies"
FT Peptide 120..125
FT /label= Immunogen

FT Peptide /note= "For production of antibodies"
FT 421..426
FT /label= Immunogen
FT /note= "For production of antibodies"
FT Peptide 422..427
FT /label= Immunogen
FT /note= "For production of antibodies"
FT Domain 279..490
FT /label= Fibrinogen-like domain
FT /note= "Homologous to residues 631-864 of human
FT fibrinogen alpha chain"
FT 63..253
FT /label= Amino-terminal-coiled-coil-domain
FT MISC-difference 280
FT /note= "Conserved cysteine residue"
FT MISC-difference 309
FT /note= "Conserved cysteine residue"
FT MISC-difference 432
FT /note= "Conserved cysteine residue"
FT MISC-difference 445
FT /note= "Conserved cysteine residue"
XX
PN W09940193-A1.
XX
PD 12-AUG-1999.
XX
PE 03-FEB-1999; 99WO-US02303.
XX
PR 04-FEB-1998; 98US-0018258.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Holloway JL, Shoemaker KE;
XX
XX WPI; 1999-508503/42.
DR N-PSDB; AAX80866.
XX
PT Human angiotensin homologue, ZAPO3 useful for study and regulation
of angiogenesis
XX
PS Claim 1; Page 65-67; 78pp; English.
XX
XX The present sequence is a human zapo3 protein. zapo3 protein exhibits
CC significant amino acid sequence homology to angiotensin-1 and 2. It is
CC covalently linked to a moiety chosen from affinity tags, toxins,
CC radionuclides, enzymes and fluorophores. The protein is assembled as a
CC multimer and is characterized by an amino-terminal coiled coil domain and
CC a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,
CC haematopoietic and mitogenic activity. It is useful in the study and
CC regulation of angiogenesis, and for developing inhibitors of
CC angiogenesis. It is possibly involved in modulation of endocrine-vascular
CC cell association and may be used therapeutically to stimulate the
CC revascularisation of tissue, to promote angiogenesis and prevent neuronal
CC degeneration. DNA probes and anti-zapo3 antibodies can be used to detect
CC sites of angiogenesis.
XX
SQ Sequence 491 AA;
Query Match 20.2%; Score 425; DB 20; Length 491;
Best Local Similarity 26.9%; Pred. No. 4.9e-34;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;
QY 44 SNADDESKNDVCKEDCEESCDYKTKITRE-EKHFMGRNONGSIYSTRTKILRM 102
DB 68 TKGDASTIKMTIRMDLENIKDVLSROKREIDVQLVVDGNTVNEVKILRESRMN 127
QY 103 DE-QQASIDYL-----SNQVEMLMNRVLLTTE----- 129
DB 128 SRVQLVWQLLHEIRKRDNSLELSQLENKTLNVTTELKMATRYRELEVAYASLTDLVN 187
QY 130 -----VERKQ---LDP-----FPHRPVOSHGL----- 148
DB 188 NOSVITLLEECLEIFSRDTHVSPPLVGVVPOHHPMSQGYTGLLGNEIQDPGYPR 247

XX 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-052317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
DR N-PSDB; AAH26235, AAH26236.
XX
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS Claim 10; Page 128-129; 140pp; English.

XX The present sequence is that of human secreted prothrombinase-like
CC polypeptide (PLP) mature polypeptide, as predicted from
CC polynucleotides (see AAH26235-36) derived from an ovary cDNA clone.
CC PLP polynucleotides and polypeptides, including the mature protein,
CC can be used in the diagnosis, treatment and/or prevention of diseases
CC associated with the dysregulation of coagulation pathways, such as
CC haemophilia, myocardial infarction, glomerular disease, diabetes,
CC fulminant viral hepatitis and atherosclerosis. They may also be
CC beneficial in the treatment of viral infections and some forms of
CC cancer. A claimed method of treating a subject in need of enhanced
CC PLP activity or expression involves the administration of PLP, a
CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
CC treating a subject having need to inhibit activity or expression of
CC PLP involves the administration of a PLP antagonist, a
CC polynucleotide that inhibits expression of a PLP polynucleotide,
CC or a polypeptide that competes with the PLP for its ligand. The
CC polypeptides can also be used to raise antibodies, as food
CC supplements, and to screen for agonists and antagonists.

XX Sequence 368 AA:

Query Match 100.0%; Score 2000; DB 22; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVVQNCYVHSTDDSVYIVEDGSNAKDESKSNDTVCKEDCEESCDVTKTTRREKHEMC 60
DB 1 EVVQNCYVHSTDDSVYIVEDGSNAKDESKSNDTVCKEDCEESCDVTKTTRREKHEMC 60
QY 61 RNLONSIVSTRSTKTLRNMMDEQOASLDYLSNOVNEFMNRVLLTTEVFRKOLDPPH 120
DB 61 RNLONSIVSTRSTKTLRNMMDEQOASLDYLSNOVNEFMNRVLLTTEVFRKOLDPPH 120
QY 121 RPYVSHGLDCTDIDKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYGGGVTYIQKRID 180
DB 121 RPYVSHGLDCTDIDKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYGGGVTYIQKRID 180
QY 181 GIIFQRLMCTYLDGFGDLGEFVLGLKKIITYNQKNTSEMLYVLALESDDTLAYASYD 240
DB 181 GIIFQRLMCTYLDGFGDLGEFVLGLKKIITYNQKNTSEMLYVLALESDDTLAYASYD 240
QY 241 NEWLEDEFRPFKMLGRYSGNAGDAFRGLKKEDNONAMPFSVDVNDGCRACIYVNGOS 300
DB 241 NEWLEDEFRPFKMLGRYSGNAGDAFRGLKKEDNONAMPFSVDVNDGCRACIYVNGOS 300
QY 301 VKSCSHLANKTGWPFNECGLANLNGIHHSGLKATATGIGWGTWTKNNSPVKIKYSMKIR 360
DB 301 VKSCSHLANKTGWPFNECGLANLNGIHHSGLKATATGIGWGTWTKNNSPVKIKYSMKIR 360
QY 361 RMYNPFYK 368
DB 361 RMYNPFYK 368

RESULT 2
AAB82584
ID AAB82584 standard; Protein; 368 AA.
XX
AC AAB82584;
XX
DT 02-OCT-2001 (first entry)
XX
XX Human prothrombinase-like polypeptide.
DE Prothrombinase-like polypeptide; human; haemostatic; cardiant;
XX nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW antiatherosclerotic; antitumor; vulnerary; osteoporosis;
KW immunomodulatory; antineumatic; antiarthritic; antiinflammatory;
KW thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Protein 21..368
FT /label= Mature_protein
FT Domain 181..217
FT /note= "separately claimed in Claim 10"
FT Domain 222..234
FT /note= "fibrinogen beta/gamma chain"
FT Domain 271..285
FT /note= "separately claimed in Claim 10"
FT Domain 324..353
FT /note= "separately claimed in Claim 10"
FT Domain 324..353
FT /note= "fibrinogen beta/gamma chain"
FT /note= "separately claimed in Claim 10"
XX WO200153456-A2.
XX
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35061.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-052317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
DR N-PSDB; AAH26235, AAH26236.
XX
XX Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
PT
PS Claim 10; Page 126-127; 140pp; English.

The present sequence is that of a novel human secreted
prothrombinase-like polypeptide (PLP). The polypeptide has a
predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid
sequence similarity to human prothrombinase fgl2 protein. The
sequence was predicted from polynucleotides (see AAH26235-36)
derived from a human ovary cDNA clone. PLP polynucleotides and
polypeptides, including the mature protein, polypeptides including
PLP fibrinogen chains, and a soluble splice variant (see AAB82590),
can be used in the diagnosis, treatment and/or prevention of diseases
associated with the dysregulation of coagulation pathways, such as

CC haemophilia, myocardial infarction, glomerular disease, diabetes,
 CC fulminant viral hepatitis and atherosclerosis. They may also be
 CC beneficial in the treatment of viral infections and some forms of
 CC cancer. A claimed method of treating a subject in need of enhanced
 CC PLP activity or expression involves the administration of PLP, a
 CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
 CC treating a subject having need to inhibit activity or expression of
 CC PLP involves the administration of a PLP antagonist, a
 CC polynucleotide that inhibits expression of a PLP polynucleotide,
 CC or a polypeptide that competes with the PLP for its ligand. The
 CC polypeptides can also be used to raise antibodies, as food
 CC supplements, and to screen for agonists and antagonists.

XX Sequence 388 AA;

Query Match 100.0%; Score 2000; DB 22; Length 388;
 Best Local Similarity 100.0%; Pred. No. 2e-195;
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVVQNCVHSTSSVNIIVEDGSNAKDESKNDTVCKEDCESCDVTKITREKHFMC 60
 DB 21 EVVQNCVHSTSSVNIIVEDGSNAKDESKNDTVCKEDCESCDVTKITREKHFMC 80
 QY 61 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVERKQIDPPRH 120
 DB 81 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVERKQIDPPRH 140
 QY 121 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYRGGWTYQKRID 180
 DB 141 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYRGGWTYQKRID 200
 QY 181 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYIVNQKTSFMLYVALESEDDTLAYASYD 240
 DB 201 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYIVNQKTSFMLYVALESEDDTLAYASYD 260
 QY 241 NFWLEDETRFFKMLGRYSNAGAPRGLKEDNOMNPFSTSYDNDGCRPACIVNQS 300
 DB 261 NFWLEDETRFFKMLGRYSNAGAPRGLKEDNOMNPFSTSYDNDGCRPACIVNQS 320
 QY 301 VKSCSHLHNTGWFNNECGLANLNGIHFSGLKATGIOMGTWTKNNSPVKIKSVSMKIR 360
 DB 321 VKSCSHLHNTGWFNNECGLANLNGIHFSGLKATGIOMGTWTKNNSPVKIKSVSMKIR 380
 QY 361 RMYNRYFK 368
 DB 381 RMYNRYFK 388

RESULT 3

AAV72622 standard; Protein; 388 AA.

XX AAV72622;

XX 02-MAY-2001 (first entry)

DE Human angiotensin protein, CG144.

XX Human: angiotensin; angiotensin; gene therapy; CG144;
 KW vascular stability; neovascularisation; nutritional supplement; therapy;
 KW myocardial infarction; proliferative retinopathy; atherosclerosis;
 KW coronary heart disease; arterial ischaemia; bone disorder; cancer;
 KW abnormal vascular growth; anaemia; chronic inflammation; immune disorder;
 KW haematopoiesis related disorder; coagulation disorder; leukaemia;
 KW cytosolic; vasotropic; food supplement; nervous system disorder;
 KW drug screening.

XX Homo sapiens.

XX Key location/Qualifiers

FT Peptide 1..22
 FT /label= Signal_peptide
 FT Protein 23..388

FT Domain /note= "Mature angiotensin protein, CG144"
 FT 193..230
 FT /note= "Fibrinogen domain"
 FT 234..247
 FT /note= "Fibrinogen domain"
 FT 283..301
 FT /note= "Fibrinogen domain"
 FT 307..321
 FT /note= "Fibrinogen domain"
 FT 337..366
 FT /note= "Fibrinogen domain"

XX WO200105825-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-US19429.

XX 16-JUL-1999; 99US-0354881.

XX (HYSE-) HYSEQ INC.

XX Ballinger DG, Montgomery JR;

XX WPI: 2001-091966/10.

XX N-PSDB: AAD02607.

PT Human angiotensin protein and DNA encoding sequences useful for
 PT preventing, creating or ameliorating a medical condition in a mammalian
 FT subject e.g. arthritis and cancer -
 PS Claim 10: Page 111-112; 132pp; English.

XX The present sequence is human angiotensin protein, CG144.
 CC The present invention relates to human angiotensin polypeptides such
 CC as CG006, CG007, CG015, CG144 and CG250. The angiotensin polynucleotides
 CC are used as hybridisation probes, for chromosome and gene mapping, to
 CC identify polymorphism and for recombinant protein production.
 CC Angiotensin may be useful for modulating vascular stability and
 CC neovascularisation associated with various pathologies. It is used as a
 CC nutritional supplement, molecular weight marker and in gene therapy. It
 CC is also used for preventing, treating or ameliorating angiogenesis
 CC related disorders such as myocardial infarction, proliferative
 CC retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia,
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,
 CC anaemia and chronic inflammation (e.g., asthma and arthritis) and immune
 CC disorders (e.g., inflammatory reactions and autoimmune diseases),
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell
 CC deficiencies), coagulation disorders, leukaemias and nervous system
 CC disorders. It is also used in drug screening techniques for screening
 CC compounds which are able to modulate the expression or activity of
 CC angiotensin. The compounds can also be used to treat diseases and
 CC disorders.

XX Sequence 388 AA;

Query Match 99.8%; Score 1996; DB 22; Length 388;
 Best Local Similarity 99.7%; Pred. No. 5.2e-195;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVVQNCVHSTSSVNIIVEDGSNAKDESKNDTVCKEDCESCDVTKITREKHFMC 60
 DB 21 EVVQNCVHSTSSVNIIVEDGSNAKDESKNDTVCKEDCESCDVTKITREKHFMC 80
 QY 61 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVERKQIDPPRH 120
 DB 81 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVERKQIDPPRH 140
 QY 121 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYRGGWTYQKRID 180
 DB 141 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYRGGWTYQKRID 200
 QY 181 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYIVNQKTSFMLYVALESEDDTLAYASYD 240

DB 201 GIIDFQRLMCDYLDGFDLGEFWMGLKIFIVYNOKNTSFMLYVALESEDDTLAAYSD 260
QY 241 NFWLEDETRFEFKMLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 300
DB 261 NFWLEDETRFEFKMLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 320
QY 301 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLLATGIGMTWTKNNSPVKIKSVSMKIR 360
DB 321 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLLATGIGMTWTKNNSPVKIKSVSMKIR 380
QY 361 RMYNPFYK 368
DB 381 RMYNPFYK 388

RESULT 4
AB877546
ID AB877546 standard; Protein; 388 AA.
XX
AC AB877546;
XX
DT 05-AUG-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2.
XX
KW Human; collagen II; aggrecan; antiarthritic; cartilage;
XX arthritits deformans.
XX
OS Homo sapiens.
XX
PN WO200242448-A1.
XX
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-JP10150.
XX
PR 22-NOV-2000; 2000JP-0356378.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Yaenunaga K;
XX
PI WPI: 2002-463631/49.
XX
DR N-PSDB: ABL60374.
XX
PT Human polypeptide promoting collagen II and aggrecan production for
XX treatment and prevention of arthritis deformans.
XX
PS Claim 1; Page 56-57; 72pp; Japanese.
XX
CC The invention relates to human polypeptide (AB877546) promoting collagen
XX II and/or aggrecan activity created by addition, deletion and/or
XX substitution. The polypeptide has antiarthritic activity and promotes
XX collagen II and aggrecan production in cartilage cells. It is useful for
XX treatment and prevention of arthritis deformans.
XX
SQ Sequence 388 AA:
XX
Query Match 99.1%; Score 1982; DB 23; Length 388;
Best Local Similarity 99.5%; Pred. No. 1,4e-193;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYVQNCNCHSTSDSVYVIVEDGSSNAKDSKNDYCKKDCESCDDYKTKITREEKHEMC 60
DB 21 EYVQNCNCHSTSDSVYVIVEDGSSNAKDSKNDYCKKDCESCDDYKTKITREEKHEMC 80
QY 61 RULQNSIYVSTSTKRLKLNMDDEOASLDYLSNOYNEIMNRYLLITTEVFRKQLDPFH 120
DB 81 RULQNSIYVSTSTKRLKLNMDDEOASLDYLSNOYNEIMNRYLLITTEVFRKQLDPFH 140
QY 121 RYVQSHGLDCTDIDKIDTIGSVTKPSGLYIIEGSSYPFEVACMDMYRGSGWTVIQRI 180

DB 141 RYVQSHGLDCTDIDKIDTIGSVTKPSGLYIIEGSSYPFEVACMDMYRGSGWTVIQRI 200
QY 181 GIIDFQRLMCDYLDGFDLGEFWMGLKIFIVYNOKNTSFMLYVALESEDDTLAAYSD 240
DB 201 GIIDFQRLMCDYLDGFDLGEFWMGLKIFIVYNOKNTSFMLYVALESEDDTLAAYSD 260
QY 241 NFWLEDETRFEFKMLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 300
DB 261 NFWLEDETRFEFKMLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 320
QY 301 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLLATGIGMTWTKNNSPVKIKSVSMKIR 360
DB 321 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLLATGIGMTWTKNNSPVKIKSVSMKIR 380
QY 361 RMYNPFYK 368
DB 381 RMYNPFYK 388

RESULT 5
AAB82593
ID AAB82593 standard; Protein; 306 AA.
XX
AC AAB82593;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant mature protein.
XX
KW Prothrombinase-like polypeptide: human; haemostatic; cardiac;
XX nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
XX antiatherosclerotic; antiulcer; vulnerary; osteoporosis;
XX immunomodulatory; antineumatic; antiarthritic; antiinflammatory;
XX thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200153456-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35061.
XX
PR 21-JAN-2000; 2000US-0488725.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PR 25-APR-2000; 2000US-0552317.
XX
PR 17-JUN-2000; 2000US-0596196.
XX
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX Arterburn MC, Tang YT, Liu C, Drmanac R;
XX WPI: 2001-483140/52.
XX
DR N-PSDB: AAH26237.
XX
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
XX diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS Claim 10; Page 135-136; 140pp; English.
XX
CC The present sequence is that of the mature portion of a novel
XX secreted, soluble splice variant (see AAB82590) of novel human
XX prothrombinase-like polypeptide (PUP). PUP polynucleotides and
XX polypeptides, including those comprising the mature protein of the
XX PUP splice variant, can be used in the diagnosis, treatment and/or
XX prevention of diseases associated with the dysregulation of
XX coagulation pathways, such as haemophilia, myocardial infarction,
XX glomerular disease, diabetes, fulminant viral hepatitis and
XX atherosclerosis. They may also be beneficial in the treatment of
XX viral infections and some forms of cancer. A claimed method of
XX treating a subject in need of enhanced PUP activity or expression

CC Involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.

XX Sequence 306 AA;

Query Match 81.2%; Score 1625; DB 22; Length 306;
Best Local Similarity 83.2%; Pred. No. 3e-157; Indels 62; Gaps 1;
Matches 306; Conservative 0; Mismatches 0;

QY 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
DB 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
QY 61 RNLQNSIVSYRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
DB 61 RNLQNSIVSYRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
QY 121 RPVQSHGLDCTDKDTIGSVTKTPSGLYIHPRESSYFEVCMCDMDYRGCGWTYQKRID 180
DB 121 RPVQSHGLDCTDKDTIGSVTKTPSGLYIHPRESSYFEVCMCDMDYRGCGWTYQKRID 180
QY 181 GIIDFQRLMCDYLDGFDDLGEFMLGLKPIFYVQKNTSPMLVYALESEDDTLAYASYD 240
DB 181 GIIDFQRLMCDYLDGFDDLGEFMLGLKPIFYVQKNTSPMLVYALESEDDTLAYASYD 240
QY 241 NFWLEDETRFPMHGLRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTLVNGQS 300
DB 241 NFWLEDETRFPMHGLRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTLVNGQS 300
QY 301 VKSCSHLHNTGWFNCEGLANLNGIHFSCKLLATGIGQGTWTKNNSPVKIKSVSMKIR 360
DB 301 VKSCSHLHNTGWFNCEGLANLNGIHFSCKLLATGIGQGTWTKNNSPVKIKSVSMKIR 360
QY 361 RMTNPFYK 368
DB 299 RMTNPFYK 306

RESULT 6
AAU14275
AAU14275 standard; protein; 326 AA.

XX AAU14275;
XX 24-OCT-2001 (first entry)
XX Human novel protein #146.
XX Human; novel protein; Antianemic; osteopathic; antiinflammatory;
XX immunomodulatory; cytosolic; neuroprotective; vulnerrary; noctropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatoprotective; haemostatic; antisthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.
XX Homo sapiens.
XX OS
XX PN WO200155437-A2.
XX PD 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02623.
XX PF 25-JAN-2000; 2000US-0491404.
XX PR
XX PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-451939/48.
XX DR N-P-SDB; AAS22580.
XX

PT isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 605; 894pp; English.

CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/ elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.

XX Sequence 326 AA;

Query Match 81.2%; Score 1625; DB 22; Length 326;
Best Local Similarity 83.2%; Pred. No. 3.3e-157; Indels 62; Gaps 1;
Matches 306; Conservative 0; Mismatches 0;

QY 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
DB 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 80
QY 61 RNLQNSIVSYRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
DB 61 RNLQNSIVSYRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 140
QY 121 RPVQSHGLDCTDKDTIGSVTKTPSGLYIHPRESSYFEVCMCDMDYRGCGWTYQKRID 180
DB 121 RPVQSHGLDCTDKDTIGSVTKTPSGLYIHPRESSYFEVCMCDMDYRGCGWTYQKRID 200
QY 181 GIIDFQRLMCDYLDGFDDLGEFMLGLKPIFYVQKNTSPMLVYALESEDDTLAYASYD 240
DB 201 GIIDFQRLMCDYLDGFDDLGEFMLGLKPIFYVQKNTSPMLVYALESEDDTLAYASYD 220
QY 241 NFWLEDETRFPMHGLRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTLVNGQS 300
DB 221 NFWLEDETRFPMHGLRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTLVNGQS 258
QY 301 VKSCSHLHNTGWFNCEGLANLNGIHFSCKLLATGIGQGTWTKNNSPVKIKSVSMKIR 360
DB 259 VKSCSHLHNTGWFNCEGLANLNGIHFSCKLLATGIGQGTWTKNNSPVKIKSVSMKIR 318
QY 361 RMTNPFYK 368
DB 319 RMTNPFYK 326

RESULT 7

AAU14511
ID AAU14511 standard; Protein: 326 AA.
XX
AC AAU14511;
XX
DT 24-OCT-2001 (first entry).
XX
DE Human novel protein #382.
XX
KW Human: novel protein; Antianaemic; osteopathic; antiinflammatory;
KW Immunomodulatory; cytostatic; neuroprotective; vulnerrary; noctropic;
KW aminconvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antilepteric; dermatological; haemostatic; antisthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-451939/48.
DR N-PSDB: AAS22816.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4; Page 848-849; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumor, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.
XX
SQ Sequence 326 AA;
Query Match 81.2%; Score 1625; DB 22; Length 326;
Best Local Similarity 83.2%; Pred. No. 3,3e-157;
Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
QY 1 EVVQNCVHSHSTDSVYVIVEDGSAKDESKSNDTVCKEDCESCDVTKITREKHEMC 60
|||||

DB 21 EVVQNCVHSHSTDSVYVIVEDGSAKDESKSNDTVCKEDCESCDVTKITREKHEMC 80
QY 61 RNLQNSIVSYSTRSKLLFNMDDEQASLDYLSNOVNEIMANRVLLTTEVERKQDPEPH 120
DB 81 RNLQNSIVSYSTRSKLLFNMDDEQASLDYLSNOVNEIMANRVLLTTEVERKQDPEPH 140
QY 121 RPYQSHGLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPEVWCDDYRGSGWTVIQKRID 180
DB 141 RPYQSHGLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPEVWCDDYRGSGWTVIQKRID 200
QY 181 GIIDFQRLMCDYLDGFGDILGEFWLGKRIFYIVNQKNTSFMLYALASEDDTLVASYD 240
DB 201 GIIDFQRLMCDYLDGFGDILGEFWLGKRIFYIVNQKNTSFMLYALASEDDTLVASYD 220
QY 241 NFWLEDETRFEKMHIGRYSGNAGDAFRGLKKEDQNNAMFSTSDVNDGCRPACLVNGQS 300
DB 221 -----GDAFRGLKKEDQNNAMFSTSDVNDGCRPACLVNGQS 258
QY 301 VKSCSHLHNTGTGMPNECGLANLNGIHFSGLKLTATGLOWGTWTKNSPVKIKSYSMKIR 360
DB 259 VKSCSHLHNTGTGMPNECGLANLNGIHFSGLKLTATGLOWGTWTKNSPVKIKSYSMKIR 318
QY 361 RMYNPFYK 368
DB 319 RMYNPFYK 326
RESULT 8
AAB82590
ID AAB82590 standard; Protein: 326 AA.
XX
AC AAB82590;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant.
XX
KW Prothrombinase-like polypeptide; human; haemostatic; cardiant;
KW nephrotropic; antidilabetic; hepatotropic; antiviral; cytostatic;
KW antilarteriosclerotic; antiallergic; vulnerrary; osteoporosis;
KW immunomodulatory; antineumatic; antiarthritic; antiinflammatory;
KW thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= "Signal peptide
FT /note= "separately claimed in Claim 10"
FT Protein 21..326
FT /label= "Mature protein
FT /note= "separately claimed in Claim 10"
FT Domain 181..217
FT /note= "fibrinogen beta/gamma chain"
FT Domain 262..292
FT /note= "fibrinogen beta/gamma chain"
FT Domain 82..321
FT /note= "blood coagulation domain, separately
FT claimed in Claim 10"
XX
PD WO200153456-A2.
XX
PE 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35061.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-0552317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
PA (HYSE-) HYSEQ INC.

RESULT 11
AAB82592 standard; Protein: 240 AA.
XX
AC AAB82592:
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant domain.
XX
KW Prothrombinase-like polypeptide: human; haemostatic; cardiac;
KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW antileukosclerotic; antitumor; vulnery; osteoporosis;
KW immunomodulatory; antirheumatic; antithrombotic; antiinflammatory;
KW thrombolytic; diagnosis; therapy; blood coagulation.
XX
OS Homo sapiens.
XX
XX WO200153456-A2.
XX
XX 26-JUL-2001.
XX
XX PD 22-DEC-2000; 2000WO-US35061.
XX
XX PF 21-JAN-2000; 2000US-0488725.
XX
XX PR 25-JAN-2000; 2000US-0491404.
XX
XX PR 25-APR-2000; 2000US-0552317.
XX
XX PR 17-JUN-2000; 2000US-0596196.
XX
XX PR 31-AUG-2000; 2000US-0643313.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX Arterburn MC, Tang YT, Liu C, Drmanac R;
XX WPI: 2001-483140/52.
XX
XX DR N-PSDB; AAS826237.
XX
XX PT Novel prothrombinase-like polypeptides and polynucleotides useful in
XX diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX PS Claim 10; Page 134-135; 140pp; English.
XX
XX CC The present sequence is that of the blood coagulation domain of a
XX secreted, soluble splice variant (see AAB82590) of novel human
XX prothrombinase-like polypeptide (PLP). PLP polynucleotides and
XX polypeptides, including those comprising the present domain of the
XX PLP splice variant, can be used in the diagnosis, treatment and/or
XX prevention of diseases associated with the dysregulation of
XX coagulation pathways, such as haemophilia, myocardial infarction,
XX glomerular disease, diabetes, fulminant viral hepatitis and
XX atherosclerosis. They may also be beneficial in the treatment of
XX viral infections and some forms of cancer. A claimed method of
XX treating a subject in need of enhanced PLP activity or expression
XX involves the administration of PLP, a PLP agonist or a
XX polynucleotide encoding PLP. A claimed method of treating a subject
XX having need to inhibit activity or expression of PLP involves the
XX administration of a PLP antagonist, a polynucleotide that inhibits
XX expression of a PLP polynucleotide, or a polypeptide that competes
XX with the PLP for its ligand. The polypeptides can also be used to
XX raise antibodies, as food supplements, and to screen for agonists
XX and antagonists.
XX
XX SQ Sequence 240 AA;
XX
XX Query Match 63.2%; Score 1265; DB 22; Length 240;
XX Best Local Similarity 79.5%; Pred. No. 1.3e-10;
XX Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
XX
OY 62 NLQNSIVYSTRKTLKLNMDDEOASLDYLSNOVNEIMNRYLLTTEVFRKOLDPPFHR 121
DB 1 NLQNSIVYSTRKTLKLNMDDEOASLDYLSNOVNEIMNRYLLTTEVFRKOLDPPFHR 60

OY 122 PVQSHGLDCTDIDKDTIGSVTKTPSGLYTIHPEGSSYPPEVNCMDMDYRGCGMTVIQKRIDG 181
DB 61 PVQSHGLDCTDIDKDTIGSVTKTPSGLYTIHPEGSSYPPEVNCMDMDYRGCGMTVIQKRIDG 120
OY 182 IIDFQRLMCDYLDGFGDLDGFEWLGKRIFYIVQKNKSPFLVYALASEDDTLAYASIDN 241
DB 121 IIDFQRLMCDYLDGFGDLDGFEWLGKRIFYIVQKNKSPFLVYALASEDDTLAYASIDN 139
OY 242 FWLEDETRFFKMHILGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRACIYNGOSV 301
DB 140 -----GDAFRGLKKEEDNONAMPSTSDVNDGCRACIYNGOSV 178
OY 302 KCSHLHNKGTWMEFNECGLANLNGIHFESGKILATGIGWGTWKNNSPVKIKYSMKIRR 361
DB 179 KCSHLHNKGTWMEFNECGLANLNGIHFESGKILATGIGWGTWKNNSPVKIKYSMKIRR 238
OY 362 MY 363
DB 239 MY 240
RESULT 12
AABG22365
ID AABG22365 standard; Protein: 141 AA.
XX
XX AABG22365:
XX
XX AC 18-FEB-2002 (first entry)
XX
XX DT 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #22356.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PT Drmanac RT, Liu C, Tang YT;
XX
XX DR WPI: 2001-639362/73.
XX
XX DR N-PSDB; AAS86552.
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX PS Claim 20; SEQ ID NO 52724; 103pp; English.
XX
XX CC The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 141 AA:
Query Match 31.7%; Score 634; DB 22; Length 141;
Best Local Similarity 64.3%; Pred. No. 1.7e-56;
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;
QY 158 PEVWCMQMDYRGSGWTVIQKRIDGIIIDFQRLMCDYLDGFGDLLGEFWLGIKKIIFYVNOK 217
DB 9 PEVWCMQMDYRGSGWTVIQKRIDGIIIDFQRLMCDYLDGFGDLL----- 51
QY 218 NPSFMYVALHESRDYLAASVDNFWLDEDTFRFKMHLGRYSGNADARGLKKEDNQA 277
DB 52 -----GDAFLFLKKEDNQA 66
QY 278 MPFSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMWFNECGLANNGIHFSGKLLATG 337
DB 67 MPFSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMWFNKGGLANNGIHFSGKLLATG 126
QY 338 IQMGT 342
DB 127 IQMGT 131
RESULT 13
ABG22361
ID ABG22361 standard; Protein; 138 AA.
XX
AC ABG22361;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22352.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS86548.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52720; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA:
Query Match 26.9%; Score 538.5; DB 22; Length 138;
Best Local Similarity 62.3%; Pred. No. 9.7e-47;
Matches 109; Conservative 0; Mismatches 1; Indels 65; Gaps 1;
QY 1 EYVQGCYVHHSTDSYVNIYEDGSNAKDSKNDYCKEDCESCYKTKITREEKHFMC 60
DB 29 EAVQGCYVHHSTDSYVNIYEDGSNAKDSKNDYCKEDCESCYKTKITREEKHFMC 88
QY 61 RNLQNSIVSYTRSTKRLRNMDQOASLDYLSNOYELMNRVLLTTEVFRQDLPFPH 120
DB 89 RNLQNSIVSYTRSTKRLRNMDQOASLDYLSNO----- 123
QY 121 RPYQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMQMDYRGSGWTVI 175
DB 124 -----VNCMDMYRGSGWTVI 138
RESULT 14
ABG22364
ID ABG22364 standard; Protein; 116 AA.
XX
AC ABG22364;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS86551.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX

PS Claim 20; SEQ ID NO 52723; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

SO Sequence 116 AA;

Query Match 26.1%; Score 521; DB 22; Length 116;
Best Local Similarity 93.1%; Pred. No. 4.6e-45;
Matches 95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 141 TKTPSGIYIHPRGSSYFVEMCDMDYRGSGWYIQKRIGIIDFORLWCDYLDGFDLL 200
DB 13 TKTPSGIYIHPRGSSYFVEMCDMDYRGSGWYIQKRIGIIDFORLWSDYLDGFDLY 72
QY 201 GEFWLGKRIFFIYNOKNTSEMLVVALESDDTLAVSYDNF 242
DB 73 GEFWLGKRIFFIYNOKNTSEMLVVALESDDTLAVSYDNF 114

RESULT 15

AA26196
ID AAY26196 standard; protein; 491 AA.

AC AAY26196;

XX 03-NOV-1999 (First entry)

DE Human zapo3 protein.

XX Human zapo3 protein; angiotensin-1; angiotensin-2; covalently linked;
KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;
KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiotensin;
KW haematopoietic; mitogenic activity; angiogenesis; inhibitor;
KW endocrine-vascular cell association; revascularisation; DNA probe;
KW neuronal degeneration; anti-zapo3 antibody.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Peptide /label= Secretory_Signal_Sequence

FT Peptide 43..48

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 93..98

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 120..125

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 421..426

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 422..427

FT /label= Immunogen

FT /note= "For production of antibodies"

FT Domain 279..490

FT /label= Fibrinogen-like domain

FT /note= "Homologous to residues 631-864 of human
fibrinogen alpha chain"

FT Domain 63..253

FT /label= Amino-terminal_coiled_coil_domain

FT MISC-difference 280

FT /note= "Conserved cysteine residue"

FT MISC-difference 309

FT /note= "Conserved cysteine residue"

FT MISC-difference 432

FT /note= "Conserved cysteine residue"

FT MISC-difference 445

FT /note= "Conserved cysteine residue"

PN WO940193-A1.

PD 12-AUG-1999.

PF 03-FEB-1999; 99WO-US02303.

PR 04-FEB-1998; 98US-0018258.

PA (ZYMO) ZYMOGENETICS INC.

PI Holloway JL, Shoemaker KE;

DR WPI; 1999-508503/42.

DR N-PSDB; AAX80866.

PT Human angiotensin homologue, ZAPo3 useful for study and regulation

PS Claim 1; Page 65-67; 78pp; English.

XX The present sequence is a human zapo3 protein. Zap3 protein exhibits
CC significant amino acid sequence homology to angiotensin-1 and 2. It is
CC covalently linked to a moiety chosen from affinity tags, toxins,
CC radionuclides, enzymes and fluorophores. The protein is assembled as a
CC multimer and is characterized by an amino-terminal coiled coil domain and
CC a carboxyl-terminal fibrinogen-like domain. Zap3 has angiogenic,
CC haematopoietic and mitogenic activity. It is useful in the study and
CC regulation of angiogenesis, and for developing inhibitors of
CC angiogenesis. It is possibly involved in modulation of endocrine-vascular
CC cell association and may be used therapeutically to stimulate the
CC revascularisation of tissue, to promote angiogenesis and prevent neuronal
CC degeneration. DNA probes and anti-zapo3 antibodies can be used to detect
CC sites of angiogenesis.

SO Sequence 491 AA;

Query Match 21.2%; Score 425; DB 20; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.7e-34;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKDESKNDYVCEKCEESCQVKTITRE-EKHFCRLQNSIYSTSTKLRLNM 82

DB 68 TKGDASTITKDMTRMDLNLKDLVLSKREIDVLQVVDGNIVNEVLRKESHNM 127

QY 83 DE-QQASLDYL-----SNQVNEANRVLLTTE----- 109

DB 128 SRVQLYQMLHETIKRDNLSLEISQLEKILAVTTMLMATRYRLEVKYASLDLVN 187

QY 110 -----VFRKO---LDP-----FPHRPVQSHGL----- 128

DB 188 NQSMITLLEQCLRIKPSRQDTHVSPPLVQVPHQHNQGYRGLGNGEIQRDGPR 247

QY 129 DCTDIKDTISGVKTP-----SGLYIHPRGSSYFV 161

DB 248 DLMPPLANSPKSPKIPPTVFINEGPKDCQAKGASHVSGLYIMIKPENSNGPMOL 307

[illegible]

Search completed: December 16, 2002, 17:34:16
Job time : 33.127 secs

•

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:58 ; Search time 15.3968 Seconds
(without alignments)
2422.587 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 NMSPSQASLFLNVCIFIG.....PVKIKSVSMKIRRMNPPYK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	19.7	439	2 I37391	fibrinogen-like pr
2	405.5	19.3	432	2 A27447	cytotoxic T-lympho
3	401.5	19.1	432	2 I56934	fibrinogen-like pr
4	397	18.9	312	2 JN0596	fibrinogen-related
5	394.5	18.8	468	1 FGB0B	fibrinogen beta ch
6	375.5	17.8	491	1 FGH0B	fibrinogen beta ch
7	371.5	17.7	437	1 FGH0B	fibrinogen beta ch
8	371.5	17.7	453	1 FGH0B	fibrinogen beta ch
9	371.5	17.7	463	2 A38463	fibrinogen gamma-A
10	370	17.6	479	2 A25052	fibrinogen beta ch
11	365	17.3	444	2 S05313	fibrinogen gamma-B
12	363	17.3	432	2 FGLMS	fibrinogen gamma c
13	353	16.8	438	2 A32670	fibrinogen gamma c
14	350.5	16.7	282	2 A35084	fibrinogen-related
15	348.5	16.6	774	2 A39832	scabrous locus (sc
16	346.5	16.5	328	2 A05299	fibrinogen beta ch
17	337.5	16.0	866	2 D44234	fibrinogen alpha c
18	330	15.7	1356	2 A45445	janusin precursor,
19	329	15.6	334	2 JC5980	fibrinogen gamma-B
20	328.5	15.6	641	1 A41932	fibrinogen alpha-I
21	327.5	15.6	1353	1 JH0675	restriction precurs
22	312	14.8	323	2 A47172	transforming growt
23	311.5	14.8	437	1 FGRTGA	fibrinogen gamma-A
24	311.5	14.8	445	1 FGRTGB	fibrinogen gamma-B
25	310.5	14.8	4135	2 T42629	tenascin-X - bovin
26	310.5	14.8	1810	1 A32230	tenascin precursor
27	304.5	14.5	1914	2 T42635	tenascin Y precurs
28	303.5	14.4	326	2 S61517	tenascin-1 precurs
29	302.5	14.4	3566	1 A40701	tenascin-X precurs

30	299	14.2	417	2 S65944	tenascin-X - pig (
31	296	14.1	220	2 S28170	tenascin homolog -
32	295	14.0	326	2 B47172	tenascin-beta - pig
33	286	13.6	860	2 I48839	tenascin-X - mouse
34	284.5	13.5	2019	1 J01322	tenascin precursor
35	283.5	13.5	4006	2 T09070	probable tenascin
36	282.5	13.4	1746	1 S19694	tenascin precursor
37	271	12.9	2201	2 A32160	tenascin-C - human
38	212.5	10.1	463	2 T15876	hypothetical prote
39	180.5	8.6	915	2 T21773	hypothetical prote
40	180.5	8.6	927	2 T21772	hypothetical prote
41	173	8.2	431	2 T29850	hypothetical prote
42	154.5	7.3	933	2 A31930	cytotactin - chick
43	128.5	6.1	452	2 T26827	cytotactin - chick
44	117	5.6	127	2 PC2036	microfibril-associ
45	110.5	5.3	4588	2 T28667	dynein beta heavy

ALIGNMENTS

RESULT 1
I37391
fibrinogen-like protein expressed in T lymphocytes (PT49) - human
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C/Accession: I37391; S47273
R:Ruegg, R.
Gene 160, 257-262, 1995
A>Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A/Reference number: I37391; MIM:95369700; PMID:7642106
A/Accession: I37391
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-439 <RES>
A/Cross-references: EMBL:Z6531; NID:G535184; PIDN:CA85298.1; PID:G535185
A/Note: Submitted to the EMBL Data Library, August 1994
C/Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	19.7%	Score 413.5;	DB 2;	Length 439;
Best Local Similarity	30.2%	Pred. No. 8.6e-25;		
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Gaps 15;
QY	34	SSVNIYEDGSMADKESKNDVCKEDQ-----ESCQYKTK 70		
DB	73	SRIEVEKVEONLKEIYNLSKKSC-QDCKIADQADNGPGRNGLLPSTGAPGEVGDNRVR 131		
QY	71	ITREKHFMCNLTNS---IVSYRSTKTLRNM-----MDEQASLDYLSNQVVELM 120		
DB	132	ELSEVKNLSELSKNAKEIIVLHGRLEKLNLYVMNNIENYVDSKVNLFVFNVSIDGKC 191		
QY	121	NRVLLITTEVFRKQLDPPHPPVOSHGL--DCTDIKPTIGSVKTPSGLYIHPGSSYP 178		
DB	192	SKC-----PSQEOIQSRPVQ-HLIYKDCSDY---AIGRSSEIYRVTPDPNNS 237		
QY	179	FEVNCDDYRGCGWTYVIOKRIDGIIDFQRLMCDYLDGFGDLGFEWGLKIFPIYVQNK 238		
DB	238	FEVYCDHEMGGWTVLQARLDGSTNFTKWQDYKAGFNIRREFWGLNDKIHILT--KS 295		
QY	239	TSPMLVYALSEDDTLAYASYDNFMLEDETRFFKMLGRYSGNAGDAFRLKKEDNONAM 298		
DB	296	KEMILRIDLEDENFVCELYALDYQEVYANFELKYRLHYGVNNGTAGDALR-FNKRYNNDLK 354		
QY	299	PFSTSDVDNOCGRACLVNGOSVYKCSHLNKKTKTWNEEGCLANDG-IHFSKLLATG 357		
DB	355	FTTPPDKDNDRYPSG-----NCG-LYSSGWPADCLASNLNGKYYHOKYRGVRNG 404		
QY	358	IOMGTW--TKNNSPVKIKSVSMKIRRMNPPYK 388		
DB	405	IFMGTWPGVSAHAGGYSKSEKAKMIRPKHRK 438		

RESULT 2

A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haseg, M.G.; Toneyama, S.; Salto, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:8717527; PMID:3550794
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <ORF>
A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.3%; Score 405.5; DB 2; Length 432;

Best Local Similarity 35.4%; Pred. No. 3.6e-24;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNLNRRVLLTTEVERKQD-----PPF 139

DB 137 LKNADQIOGLQGRLETLHLVMNNIENVYDNKRVANLTVV--NSLDGCKSPQSEHMQ 194

QY 140 HRPVQSHG--DCTDIKDTIGSVTPPSGLYIIHPEGSSYPPEVWCMDYRGGGTVIOL 197

DB 195 SQPVQ-HLIYKDCSD-HYVLG---RRSSGAYRVTPDHRNSFEVYCDMETMGGGTVIQA 249

QY 198 RIDGIDFQRLMCDYLDGFDLIGEFWLGKIKFIYVNOKNTPSMILYVALESDDTLAYA 257

DB 250 RLDSGTNTRKMKDYKAGAGNLEREFWLGNDKIHLLT--KSEMLIRIDLEFNGILTLYA 307

QY 258 SYDNWLEDETRFFKMHILGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 317

DB 308 LYDOFYVANEFLKYRLHIGNYNGTGADALR-PSRHYNHDLRFETTPDRNDRYPSG---- 362

QY 318 GQSVSCSHLNKTKTGMWNEGCLANLNG-IHFGSKLLATGLOMGTWTKNN--SPVKIKS 374

DB 363 -----NCG-LYSSGWMWDSCLSNLNGKYYHQKYGVRNGIFGTWPGINAOPEGYKS 416

QY 375 VSMKIRMYNP 385

DB 417 SFKQAKMIRP 427

RESULT 3

I56934
fibrinogen-like protein - mouse

C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934

R:Parf, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995

A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus induce

A:Reference number: I56934; MUID:95333285; PMID:7609073

A:Accession: I56934

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-432 <RES>

A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAA34823.1; PID:g1042170

C:Genetics:

A:Gene: musfibp

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.1%; Score 401.5; DB 2; Length 432;
Best Local Similarity 35.0%; Pred. No. 7.4e-24;
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNLNRRVLLTTEVERKQD-----PPF 139

DB 137 LKNADQIOGLQGRLETLHLVMNNIENVYDNKRVANLTVV--NSLDGCKSPQSEHMQ 194

QY 140 HRPVQSHG--DCTDIKDTIGSVTPPSGLYIIHPEGSSYPPEVWCMDYRGGGTVIOL 197

DB 195 SQPVQ-HLIYKDCSD-HYVLG---RRSSGAYRVTPDHRNSFEVYCDMETMGGGTVIQA 249

QY 198 RIDGIDFQRLMCDYLDGFDLIGEFWLGKIKFIYVNOKNTPSMILYVALESDDTLAYA 257

DB 250 RLDSGTNTRKMKDYKAGAGNLEREFWLGNDKIHLLT--KSEMLIRIDLEFNGILTLYA 307

QY 258 SYDNWLEDETRFFKMHILGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 317

DB 308 LYDOFYVANEFLKYRLHIGNYNGTGADALR-PSRHYNHDLRFETTPDRNDRYPSG---- 362

QY 318 GQSVSCSHLNKTKTGMWNEGCLANLNG-IHFGSKLLATGLOMGTWTKNN--SPVKIKS 374

DB 363 -----NCG-LYSSGWMWDSCLSNLNGKYYHQKYGVRNGIFGTWPGINAOPEGYKS 416

QY 375 VSMKIRMYNP 385

DB 417 SFKQAKMIRP 427

RESULT 4

JN0596
fibrinogen-related protein HRP-1 precursor - human

C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596

R:Yamamoto, T.; Golob, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993

A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related

A:Reference number: JN0596; MUID:95290661; PMID:8390249

A:Accession: JN0596

A:Molecule type: mRNA

A:Residues: 1-312 <YAM>

A:Cross-references: GB:D14446; NID:g939314; PIDN:BA03336.1; PID:g939315

A:Experimental source: liver

C:Superfamily: fibrinogen beta/gamma homology

F:18-312/Domain: signal sequence #status predicted <SIG>

F:18-312/Product: fibrinogen-related protein HRP-1 #status predicted <MAT>

F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.9%; Score 397; DB 2; Length 312;

Best Local Similarity 34.3%; Pred. No. 1.1e-23;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 87 IVSYSTRKLLRNMMDEQAQSLDLSNQVNLNRRVLLTTEVERKQ----- 134

DB 4 VPSFLVTVTALL---MGRISALDECAQOMLRANQVRLLETRVAKQOQYKIKQLQENYV 60

QY 135 --LDPEPHRPVQSHG-----LDCTDIKDTIGSVTPPSGLYIIHPEGSSYPPEVWCMDY 187

DB 61 QFLDGDDEDETVVLDLSKROYADCEIFNDGYKL-----SGFYKIKPLQSPAFPSYVCDMS- 115

QY 188 RGGGTVIOLKRIIDGIIIDPQRLMCDYLDGFDL---GEWGLGKIKFIYVNOKNTPSMILY 244

DB 116 DGGGTVIOLKRIIDGIIIDPQRLMCDYLDGFDL---GEWGLGKIKFIYVNOKNTPSMILY 244

QY 245 VALESEDDTLAASYNDFLEDETRFFKMHILGRYSGNAGDAFRGLKEDNQ-----NAMP 299

DB 174 IDLAFPEKSKRYAQYKKNFYVDEKKNFYELNIGYSGTACDSLAGFHEPEVOMWASHORMK 233

QY 300 FSTSDVNDGCRPACLVNQSVKCSHLNKTGMWFNEGCLANLNGIHHFGSKLLA--T 356

DB 234 FSTWDRHDHNYEGNCAEEDS-----GMWFNRCHSANLNGV-YISGPTAKTDN 281

QY 357 GIOMGTWTKNNSPVAKISKMKIR 380

DB 282 GIVWYTW--HGWWYSIKSVYMKIR 303

RESULT 5

FGBOB

```

fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence, revision 28-Jul-1981 #text, change 13-Sep-1996
C:Accession: A03122; B03117; B37507; A37513; S02443
R:Biomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A>Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: protein
A:Residues: 1-4 <BLD>
R:Sjogquist, J.; Biomback, B.; Wallen, P.
Ark. Kent 16, 425-436, 1960
A>Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A>Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinogen
A:Reference number: A37507; MUID:79164394; PMID:434821
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A>Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A:Reference number: A37513; MUID:81199473; PMID:6262803
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A>Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; MUID:88211875; PMID:2966748
A:Accession: S02443
A:Molecule type: protein
A:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide B
C:Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C:Superfamily: fibrinogen beta chain, fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
F:215-464/Domain: fibrinogen beta/gamma homology <FBG>
F:215-464/Domain: fibrinogen beta/gamma homology <FBG>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F:31/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:312-313/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match      18.8%   Score 394.5; DB 1; Length 468;
Best Local Similarity 27.5%; Pred. No. 2,9e+23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;.

Oy 27 CVHSTDSVVNIYEDGSNADESKSDNTVCEDCESDVKTITREKHF--MCRNIQ 84
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Db 72 CLHADPDLGVL-----CPTCKRIODPLVRQERPIRKSIETDLR 108
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Oy 85 NSIYSYTSTK-----LLRNMDAQASLDLYSLNOYNELMN----- 121
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Db 109 NTIVSVSTSSSTFOYITLLNMKGRONOVDENENVNERSSHLEKHQLYIDETVKNNI 168
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Oy 122 -----RVLLTFTEVFRKOLDPP-----RRPVOSHGLDCTDIKDITGS 159
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Db 169 PTKLRLVASIIENLRSKIQKLESYSTQMEYCRRPCITYTCNIPVS--GKECEKITIRNGE 227
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Oy 160 VTKTPSGLIYIHPESSYPFEVMCDMDYRGGMWTVYIKRIIGIIDFORLMQDYLDGFGL 219
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Db 228 T-----SEMYTLIOPEBSSAPRYCYGDMKTEKGGMWLYIQNRQSGSLDFGKNMPYKQFPNI 283
    ||| :|| :| | | | | | | | | | | | | | | | | | | | | | | |
Oy 220 L-----GEFTGLKFIETYINOKNTSEMLYVALESDDTFLAYASTDNFWLEDE 267

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[illegible]

A:Residues: 31-112, 'E', 114-137, 'Q', 140-144, 'Q', 147-148 <BLO>
 R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201; PMID:8117655
 A:Accession: G54223
 A:Molecule type: protein
 A:Residues: 164-174 <RUN>
 A:Note: Identification of tryptic peptides from high-density lipoproteins
 R:Henschen, A.; Lotzpeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A:Title: Covalent structure of fibrinogen.
 A:Reference number: A90037; MUID:83254370; PMID:6575689
 A:Contents: annotation: review, disulfide bonds
 R:Gardlund, B.; Hessel, B.; Marguerie, G.; Mirano, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
 A:Reference number: A91249; MUID:77245999; PMID:891553
 A:Contents: annotation: disulfide bonds
 R:Doollittle, R.F.; Takagi, T.; Matt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
 A:Title: The structures of fibrinogen and their inhibitors, Magnusson, S., Ottesen, M., Fold
 A:Reference number: A94437
 A:Contents: annotation: disulfide bonds
 R:Doollittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A:Title: Fibrinogen and fibrin
 A:Reference number: A90041; MUID:84305751; PMID:6383194
 A:Contents: annotation: review, EM structure, polymerization, ligands
 R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
 Ann. N. Y. Acad. Sci. 408, 449-456, 1983
 A:Title: Cloning of fibrinogen genes and their cDNA.
 A:Reference number: A90038; MUID:83254384; PMID:6575700
 A:Contents: annotation
 R:Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A:Title: A unique proteolytic fragment of human fibrinogen containing the alpha COOH-ter
 A:Reference number: A37117; MUID:90337977; PMID:2143188
 A:Contents: annotation; hemetin cleavage site
 A:Note: hemetin, a protease from Haemeteria philianii, the giant South American leech,
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ization sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
 ger) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Genetics:
 A:Gene: GDB:FCB
 A:Cross-references: GDB:119130; OMIM:134830
 A:Map position: 4q28-4q28
 A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FC
 lns are contained in the core. Two three-chain coiled coils emerge from this core and co
 from the distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A:Pathway: blood coagulation
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
 C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic ac
 F:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
 F:31-49/Product: fibrinogen beta chain #status experimental <MAT>
 F:31-44/Product: fibrinopeptide B #status experimental <APT>
 F:45-49/Product: fibrin beta chain #status experimental <FGB>
 F:45-47/Region: polymerization site
 F:99-228/Domain: fibrinogen disulfide ring homology <FDR>
 F:28-48/Domain: fibrinogen beta/gamma homology <FBG>
 F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:95/Disulfide bonds: interchain (to alpha-55) #status experimental
 F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
 F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
 F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
 F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
 F:231-316, 241-270, 424-437/Disulfide bonds: #status experimental

F:394/Binding site: carbohydrate (asn) (covalent) #status experimental
 Query Match 17.8%; Score 375.5; DB 1; Length 491;
 Best Local Similarity 26.6%; Pred. No. 9,6e-22;
 Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;
 QY 25 GNCVHSTDSVYNNIVEDOSNAKDESKSNDYCKEDCESCVKRTPEEHFPCRNIQ 84
 DB 93 GGCLEHADPDLGVL-----CPTGCOLQELALDQE-----RPIR 124
 QY 85 NSI-----VSYTRSYK-----KLRRMMDEQASLDYLSNQVNELMN----- 121
 DB 125 NSYDELNNVNEAVSQTSSTSPQYMLLKDLMQKRQKQVNDNNVNVNYSSELEKHQLYTD 184
 QY 122 -----RVLLTTEVFRKQDPP-----NRPVQSHGLDCTD 152
 DB 185 ETVNSNIPTNLVLSILENLSKIOKLESVDASQMEYCRPTGVSCNIPVVS -GKECHE 243
 QY 153 IKDTGVSVTKTPSGYLIHDEGSSYPFEVCMQMDYRGGWYIQRIGIDIDFOLMCDY 212
 DB 244 ITRKGET---SEWLIQPDSSVVRPYRYCDMNTENGSGWYIQRNODSDYDFGRKMDPY 299
 QY 213 LDGFGD-----LLGEFWLGLKIFYIVQKNTSFMLYALSESDTLAVASYD 260
 DB 300 KGFQGVNANTDGNKYNCGLPGEWLGNDKISQLTIRGPRF--LLEEMDKDKYKAHNG 357
 QY 261 NWLEDETRFEFKMLGRSGNAGDAFRG---LKKEDN---ONAPRSTSDVNDGCRP 312
 DB 358 GFYVNEAKYKOISVNYKTAGNALMDGASOLMKEENRTYHNGMFEFSTYDRDNDG--- 414
 QY 313 ACTLVNGQSVKSCSHLHNKTKGMFNECGLANLNGIHHSFKL-----LATGIOMGTWT 364
 DB 415 --WLTSDPRKQCSK-EDGGGMWYNRCHAMPNGRYWGQYTMADAKHGTGDGVVMMWV- 470
 QY 365 KNSPVRKIKSVSMKIRMYNPFY 387
 DB 471 -KGSWYMKMKSMKIR---PFF 488
 RESULT 7
 FGBUG
 fibrinogen gamma-A chain precursor [validated] - human
 N:Alternate names: coagulation factor I
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 25-Feb-1985 #text_change 08-Dec-2000
 C:Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125;
 R:Chung, D.W.; Chan, W.Y.; Davie, E.W.
 Biochemistry 22, 3250-3256, 1983
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gam
 A:Reference number: A90470; MUID:83283434; PMID:6686357
 A:Accession: A90470
 A:Molecule type: mRNA
 A:Residues: 1-437 <CHU>
 R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
 Biochemistry 24, 2077-2086, 1985
 A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
 A:Reference number: A90494; MUID:85252774; PMID:2990550
 A:Accession: B90494
 A:Molecule type: DNA
 A:Residues: 1-113, 'T', 115-437 <RIX>
 A:Cross-references: GB:X02415; GB:M10014; NID:q182438; PIDN:AB59531.1; PID:q182439
 R:Henschen, A.; Lotzpeich, F.; Southan, C.; Topfer-Petersen, E.
 In Protides of the Biological Fluids, Proc. 28th Collloq., Peeters, H., ed., pp.51-56,
 A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structura
 A:Reference number: A94433
 A:Accession: C94433
 A:Molecule type: protein
 A:Residues: 27-437 <HEN>
 R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
 A:Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains:
 A:Reference number: A93956; MUID:83247396; PMID:6575389
 A:Accession: B93956

Oy 354 ---LATGIOMGTWTKNNSPVKIKSVSMKI 379
DB 386 PNGYDNGIIMATW--KTRWYSMKKTKTKMKI 412

RESULT 8
FCHUGB
fibrinogen gamma-B chain precursor [validated] - human
M:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
A:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R:Rikun, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774; PMID:290550
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113, 'I', 115-453 <RIX>
A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PIDN:AAB595
R:Forde, J.F., A.V.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-B fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379; PMID:6092346
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Mollenstein-Tedel, C.; Moseason, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Accession: A90453; MUID:82068993; PMID:7306501
A:Molecule type: Protein
A:Residues: 411-434, 'Y', 436-440, 'Z', 442, 'Z', 444, 'B', 446-447, 'R', 449, 'ZBP', 453 <MOU>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:88217900; PMID:3368448
A:Accession: A28203
A:Molecule type: Protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: Protein
A:Residues: 433-453 <FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334; PMID:1685103
A:Accession: I37390
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:931410; PIDN:CA53837.1; PID:9930064
C:Comment: The two forms of gamma chain, A (see PIR:FCHUG) and B, arise by alternate splicing, which makes this chain different from the gamma-B chain at positions 434-437 and C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas C:Genetics:
A:Gene: GDB:FGG
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG) lins are contained in the core. Two three-chain coiled coils emerge from this core and co from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein; F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MP>
F:126-415/Domain: fibrinogen beta/gamma homology <FBG>

F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:34/Disulfide bonds: Interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: Interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: Interchain (to beta-110) #status predicted
F:49/Disulfide bonds: Interchain (to alpha-64) #status predicted
F:78/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:161/Disulfide bonds: Interchain (to beta-227) #status predicted
F:165/Disulfide bonds: Interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

Query Match 17.7% Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 1.8e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

Oy 85 NSIVSTRSTKLLRNMDQ-----QASLYLSNQVNLNRRVLLTTEVFRKQDPF 138
DB 103 NMIDATLKSRLMLEIMKYEASILTHDSIRYLDIYNSNOKIVNLKEKV--AQLEAQ 160
Oy 139 PRPR---VQSH---GLDCTDKDTGVTKPSGLYIHPGSSYPPEWCDMDYRGGG 191
DB 161 CQEPCKDVIQIHDTGKQCD---IANKGAQSGLFIKPKAKQDFLYICEIDSGNG 216
Oy 192 WTVIOKRIDGIIIDFQRLWCVDYLDGFGD---LGEFWLGLKKFYIVNQKTSFMYVAL 247
DB 217 WTVFQKRILDSYDFKRNWYQKEGHLSPGTGTEFWLGNEXIHLISQSAIPVALREL 276
Oy 248 ESEDDTLVASYDNDWLEDETFEFKMLHGRYS-GNAGDAFRLKDED-----NQAM 298
DB 277 EDWNRSTADYAMFVKGPEADKRLTYAVFAGGAGAFDFDGDPSDKFPTSHNGM 336
Oy 299 PESTSDVDNDGCRPACLVNGQSVKCSHLHNKTMFNECGLANINGIHPFSGL----- 353
DB 337 QESTMDNDKREGCARDGS-----GMMNKKCHAGHLNGVYQGGTYSKAST 385
Oy 354 ---LATGIOMGTWTKNNSPVKIKSVSMKI 379
DB 386 PNGYDNGIIMATW--KTRWYSMKKTKTKMKI 412

RESULT 9
A38463
fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
A:Accession: A38463
R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745; PMID:2009266
A:Accession: A38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
F:73-202/Domain: fibrinogen disulfide ring homology <DBR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.7% Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 1.8e-21;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;

Oy 61 CEESDVTATKTRREKHE--MCRNLQNSIVSY--TRSTKLLRNMD----- 103
DB 80 CPTGCELTTLTKQEKTVKPVLRDLDKRAKFSPTSTMYVNMNKLKVTQKORKDN 139
Oy 104 -----EQQASLDYLSNQVNLNRRVLLTTEVFRKQDPFPHRPGS----- 145
DB 140 DIISVTEFMELEHYNITKMDLNNIPSSLVRLAVIDSL-HKRIQKLENAIATQTDYCR 198

```
QY 146 -----HGLDCTIDKDTIGSVTKPSGLYIIHPEGSSYPFEVCMDDYRGGGWT 193
DB 199 SPCVASCNIPVYSGRECEDIYRKGGET-----SEMYIIQDPDPTTPRYVYCDMETDNGGWT 254
QY 194 VIQKRIDGIIDFORLWCDYLDGFG-----DLGEFWLGLKKIRIYVQKNTSFM 242
DB 255 LIQNRQDGSVNGRAWDEYKRGFGNIAGSGKKYCDTPPEYVWAGNDKISOLYTRIGPTK-- 312
QY 243 LVVALESED---DTLAVASYDNFWELEDETRFEMHLGRYSNGNADAF---RGLAKREDN- 294
DB 313 --VLIEMEDWNGDKYS-ALYGGFTIHNEGNKYQLSVNKGNGNMLMGEASQLYGENTR 369
QY 295 ---QNAAPSTSDVDNDGCRPACLVNGQSVKSCSHLHNTGWFNEGCLANLNGIHFFSG 351
DB 370 WTIHNGMYSTYDRDNDG-----WLTTPDKKOCCK-EDGGGWVYNRCHAAHPNGRYWGG 423
QY 352 KL-----LATGIQWGTWTKNNSPVKIKSVSMKIRRMVNPYE 387
DB 424 TYSMDMAKHGTDGIVWMMN--KGSWYSMKKSMKIK---PYE 461
```

RESULT 10

```
A25052
fibrinogen beta chain - sea lamprey (fragments)
M:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
R:Bohonus, V.L.; Doollittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582; PMID:3790537
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BO>
A:Cross-references: GB:M14773; NID:9213191; PIDN:AAA9261.1; PID:9213192
R:Cottrell, B.A.; Doollittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A:Reference number: A03120; MUID:77065679; PMID:99898
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain: fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; sulfoprotein
F:1-36/Product: fibrinopeptide B #status experimental <FPB>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:90-219/Domain: fibrinogen disulfide ring homology <FBR>
F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental
```

```
Query Match 17.6%; Score 370; DB 2; Length 479;
Best Local Similarity 28.9%; Pred. No. 2.5e-21;
Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;
```

```
QY 45 NAKDESKNDYCKEDCE-----ESCDEVKTRIRREHFHFCRNQNSIVSYTRS 93
DB 130 NSFDRAASDSNTLKNVQTLRRRLNSRSSSTHVAQKEIENRYEKIR-IESTVAGSLRS 188
QY 94 TKLRNMMDDEQASLDVYLSNQVNLNMRVLLTTEVFRKQDLPFPHRPVQSHGLDCTDI 153
DB 189 MRSVLEHLAKQRMKEAIKTQ-KELCSAPCTVNCRY-----PVVS-GMHCEDI 235
QY 154 KDTIGSVTKPSGLYIIHPEGSSYPFEVCMDDYRGGGWTYQKRIDGIIDFORLWCDYL 213
DB 236 YRNGGRTSEA---YYIQDPLFSEPYKVCDFMESHGSGWTVVQNRVDSSNFARDWNTYK 291
QY 214 DENGDDL-----GEFWLGLKKIRIYVQKNTSFWLVALESDDTLAVASYDNF 262
```

```
DB 292 AEEGNIAFNGKSGICNIPGEYWLGTIVHQLTKQ-HTQOVLFDMSDEGSSV-YAQYASF 349
QY 263 WLEDETRFEMHLGRYSNGNADG-FRLGKK--BDNQ-----NAMPSTSDVDNDGCRPAC 314
DB 350 RPENEAGYRGLWVEDYSGNAGNMLLEGARIDLMGDNKRTMTIHNGMOSSTFPRDNDNRP-- 407
QY 315 LVNGQSVKSCSHLHNTGWFNEGCLANLNGIHFFSG--KLLA-----TGQWGTWTKN 366
DB 408 ---GDPTKHCSS-EDAGGWVYNRCHAAHPNGRYWGGIYTRKQADYGTDDGVVWMMN--K 461
QY 367 NSPVKIKSVSMKIR 380
DB 462 GSWYSMKQMAKLR 475
```

RESULT 11

```
S05313
fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: S05313
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A:Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibr
A:Reference number: S05313; MUID:89366676; PMID:2771651
A:Accession: S05313
A:Molecule type: mRNA
A:Residues: 1-444 <BRO>
A:Cross-references: EMBL:X15556; NID:9349; PIDN:CA433562.1; PID:9350
A:Note: The authors translated the codon AGT for residue 105 as Ala and ATT for resid
C:Superfamily: fibrinogen gamma chain: fibrinogen beta/gamma homology
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F:174-414/Domain: fibrinogen beta/gamma homology <FBG>
```

```
Query Match 17.3%; Score 365; DB 2; Length 444;
Best Local Similarity 30.2%; Pred. No. 5.7e-21;
Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;
```

```
QY 85 NSIVSYTRSRKTKLLRMNM-----DEQASLDVLSNQVNLNMRVLLTTEVFRKQDLP 138
DB 101 NNTESATKNSKSMEEITKYTELTISTHETIRLQEVYNSNSQIYNLRDKV--OLEAN 158
QY 139 PRRPVQS-----HGLDCTIDKDTIGSVTKPSGLYIIHPEGSSYPFEVCMDDYRGGG 191
DB 159 CGRPQDPTVYIHVYTGDCDD---YANKGAKSGGLFIRPL-KAQGFVLYCEIDSGNG 213
QY 192 WYIYQKRIDGIIDFORLWCDYLDGFGDL-----GEFWLGLKKIRIYVQKNTSFWLYV 245
DB 214 WYVFORLSDGSLDFKKNWIOYKKEFGHLSPGTGNTFEFWLGNKRIHLISYOSIPYLR 273
QY 246 ALLESDDTLAVASYDNFWELEDETRFEMHLGRY-SGAGAPFGLKKED-----NON 296
DB 274 QLEDMMGRTSTADYASKTVYGVNDKRYLYAVYRIGDAGAFGVDGDDSSDKFTFSHN 333
QY 297 AMPFSTSDVDNDGCRPACLVNGQSVKSCSHLHNTGWFNEGCLANLNGIHFFSGKLLAT 356
DB 334 GMGFSTWSDNDKYDNGC---AEQY-----GIGMMNKKAGHLNGVYGGCTYSKT 382
QY 357 -----GIQWGTWTKNNSPVKIKSVSMKI 379
DB 383 STPNGYDNGIIMATW--KSRWYSMKKTYMKI 411
```

RESULT 12

```
FEGLMS
fibrinogen gamma chain precursor - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 20-Oct-2000
C:Accession: A03129
R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Rile
Biochemistry 24, 92-101, 1985
A:Title: Lamprey fibrinogen gamma chain: cloning, cdna sequencing, and general charac
```


Job time : 17.3968 secs

QY	313	ACLVGCGSVSCSS-LNKTGMWNEECGLANNINGTH-FSGKLATGTIOGCTWRKNSPV	370
		::: : : ::: : : : : :	
Dd	219	-VYSINASHSSVGRAMWKSCOLLNLNGYYIDYG--APSIYSYLPGDND--	268
		::: : : ::: : : : : :	
QY	371	KIKSVSMKIR 380	
Dd	269	QIPFAEMKLR 278	
		::: : : ::: : : : : :	

RESULT 15
A39832

scabrous locus (scs) protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C:Accession: A39832, S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A:Title: Spacing differentiation in the developing *Drosophila* eye: a fibrinogen-related
A:Reference number: A39832; MUID:91075223; PMID:2175046
A:Accession: A39832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-774 <BAK>
A:Cross-references: GB:M60065; GB:M37703; MID:g158401; PID:g158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A:Title: Molecular analysis of scabrous mutant alleles from *Drosophila melanogaster* ind
A:Reference number: S58998; MUID:96109607; PMID:8647397
A:Accession: S58998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'T', 20-774 <HUX>
C:Genetics:
A:Gene: FLYBase:scs
A:Cross-references: FLYBase:FBgn0003326
C:Superfamily: fibrinogen beta/gamma homology
F_514-711/Domain: fibrinogen beta/gamma homology <FBG>

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4

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:23 ; Search time 9.2381 Seconds

(Without alignments)
1742.006 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLLFLNVCIFIG.....PVKIKSVSMKIRRMNPFYK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	19.7	439	1	Q14314 homo sapien
2	405.5	19.3	432	1	P12804 mus musculu
3	400.5	19.0	481	1	AGP1_BOVIN
4	400.5	19.0	493	1	Q91045 mus musculu
5	398	18.9	433	1	ANL2_HUMAN
6	395.5	18.8	468	1	FGL1_HUMAN
7	395	18.8	468	1	FIBB_BOVIN
8	391	18.6	498	1	AGP1_HUMAN
9	381.5	18.1	496	1	AGP2_MOUSE
10	375.5	17.8	491	1	FIBB_HUMAN
11	375.5	17.8	375	1	AGP2_BOVIN
12	374.5	17.8	496	1	AGP2_MOUSE
13	373.5	17.8	479	1	FIBB_RAT
14	371.5	17.7	453	1	FIBG_HUMAN
15	371.5	17.7	477	1	FIBB_CHICK
16	370	17.6	477	1	FIBB_PETMA
17	365	17.3	444	1	FIBG_BOVIN
18	365	17.3	432	1	FIBG_PETMA
19	360	17.1	509	1	AGP4_MOUSE
20	358	17.0	503	1	AGP4_HUMAN
21	353	16.8	438	1	FIBG_XENLA
22	351	16.7	319	1	FCN2_RAT
23	350.5	16.7	282	1	FIBA_PARPA
24	348.5	16.6	774	1	SCA_DROME
25	337.5	16.0	866	1	FIBA_HUMAN
26	335.5	15.9	741	1	FIBA_CHICK
27	332	15.8	306	1	FCN2_MOUSE
28	329.5	15.7	641	1	FIB2_PETMA
29	329	15.6	334	1	FCN1_MOUSE
30	327.5	15.6	445	1	FIBG_RAT
31	321.5	15.3	313	1	FCN2_HUMAN
32	321	15.3	255	1	MFA4_HUMAN

34	313.5	14.9	782	1	FIBA_RAT	P06399 rattus norv
35	310.5	14.8	1808	1	TENA_CHICK	P10039 gallus gall
36	308.5	14.7	326	1	FCN1_HUMAN	O00602 homo sapien
37	305.5	14.5	335	1	FCN1_RAT	Q9T58 rattus norv
38	302.5	14.4	4289	1	TENX_HUMAN	P22105 homo sapien
39	291	13.8	299	1	FCN3_HUMAN	O75636 homo sapien
40	282.5	13.4	1746	1	TENA_PIG	Q29116 sus scrofa
41	271	12.9	2201	1	TENA_HUMAN	P24821 homo sapien
42	197	9.4	137	1	AGP2_RAT	O35462 rattus norv
43	109	5.2	129	1	MEP4_BOVIN	P55918 bos taurus
44	99.5	4.7	586	1	PMEL_ARATH	O43867 arabidopsis
45	99	4.7	599	1	YAQB_SCHPO	Q10110 schizosach

ALIGNMENTS

RESULT 1
FGL2_HUMAN STANDARD: PRT: 439 AA.
ID FGL2_HUMAN
AC Q14314;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen-like protein 2 (p749).
DE Fibrinogen precursor (Fibrinogen-like protein 2) (p749).
DE FGL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Small intestine;
RC MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytela R.;
RT "Sequence of a human transcript expressed in T-lymphocytes and encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1995).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Yuvaraj S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of Hg12: the human counterpart to the mouse gene Fg12.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.; AND VARIANT G10-53.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Ozuna M., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN [4]
RP CHARACTERIZATION.
RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Argaves S., von Fliedner V., Pytela R., Ruegg C.;
RT "Characterization of human fibrinogen, a fibrinogen-like protein secreted by T lymphocytes.";
RL J. Immunol. 161:138-147(1998).
-1- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT MUCOSAL SITES.
CC
-1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC
-1- SUBCELLULAR LOCATION: Secreted.
CC
-1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC T-CELLS.
CC
-1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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```
DR EMBL: Z36531: CAA85298.1: -.
DR EMBL: AF104015: AAD10825.1: -.
DR EMBL: AF104014: AAD10825.1: JOINED.
DR EMBL: AF468959: AAL68855.1: -.
DR HSSP: P02671: 1F2D.
DR Genew: HGNC:3696: FGL2.
DR MIM: 605351: -.
DR InterPro: IPR002181: Fibrinogen_C.
DR Pfam: PF00147: Fibrinogen_C; 1.
DR SMART: SM00186: FBG; 1.
DR PROSITE: PS00514: FIBRIN-AG-C-DOMAIN; 1.
KW T-cell; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 23
FT CHAIN 24 439
FT DOMAIN 210 435
FT DISULFID 213 242
FT DISULFID 371 384
FT CARBOHYD 25 25
FT CARBOHYD 179 179
FT CARBOHYD 235 235
FT CARBOHYD 263 263
FT CARBOHYD 336 336
FT VARIANT 53 53
FT SEQUENCE 439 AA: 50228 MW: DP34656288EA9E68 CRC64:
/FTID=VAR_013066.
Query Match 19.7%; Score 413.5; DB 1; Length 439;
Best Local Similarity 30.2%; Pred. No. 2.1e-25;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;
OY 34 SSVVNIIVEGCSNAKDESKNDVCKEDC-----ESCQVKKR 70
DB 73 SIEEEVEKQVQLAKTIWLSLKKSC-QDCKLQADNGDPGRNGLLPSTGAPEVEGDNRRV 131
OY 71 ITREEKHFCRNLIQNS---IYSTRSTKLLRN-----MDEQASLDYLSNOVNEIM 120
DB 132 ELESEVNMKSLSEKNAKEINVLHGLEKLNLYNMNNIENYDSKAVANLTFVNSLDGNC 191
OY 121 NRVLLLTTEVFRKQLDPEHPVQSHGL-DCTDIKDTIGSVTKPPSGLYIIHPESSYR 178
DB 192 SKC-----PSQEOIOSRPVQ-HLYKKDCSDYV---AIGKRSSEYRVTPDPKNS 237
OY 179 FPEVMDMDYRGGGWTVYQKRIIDIFORLMCDYLDGFGDGLGEMFLGKIFLYINOKN 238
DB 238 FEYVCDMEIMGGWTVLQKRLDGSINFTTQWQYKAGFENLREMLGDKIHLTL--KS 295
OY 239 TSFMLVVALESDPTLAAVADNFMLEDETRFKMHLGRYSNAGDAFGLKKEQNQAM 298
DB 296 KEMILRIDLEDPNGVELVALYQFVANEFKLYRLHVGNYGTAGDALR-FKKHYNHDLK 354
OY 299 PSTSDVDNDGCRPACLVNGQSVKCSHLHNTGWMFNECGLANLNG-IHHSGLLATG 357
DB 355 FETTDKNDKNDRYPSG-----NCG-LYSSGWMFDACLASANLNGKYHOKYRGVRNG 404
OY 358 IOMGTW--TKNSPYKISVSMKIRMYNP-YFK 388
DB 405 IFWGTMPGVSEAHPGYKSSFEKAKMIRPKHK 438
RESULT 2
FGL2_MOUSE STANDARD; PRT; 432 AA.
AC P12804:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibrinoleukin precursor (fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```

[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cytotoxic T-cell;
RX MEDLINE=87175527; PubMed=3550794;
RA Koyama T., Hall L.R., Hasegawa S., Salto H.;
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT homology to fibrinogen beta and gamma chains."
RT Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
[2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BAH/CJ; TISSUE=peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity."
RL J. Virol. 69:5033-5038(1995).
CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1- INDUCTION: IN MACROPHAGES, DURING INJECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3) FIBRINOGEN C-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: M16238: AAA37624.1: -.
DR EMBL: M15761: AAA37624.1: JOINED.
DR EMBL: S78773: AAB34823.1: -.
DR PIR: A27447; A27447.
DR HSP: P02671; 1F2D.
DR MGD: MGI:103266; Fgl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG-C-DOMAIN; 1.
KW T-cell; Cytolysis; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
SQ SEQUENCE 432 AA: 48951 MW: 28297696CBA4782 CRC64:
Query Match 19.3%; Score 405.5; DB 1; Length 432;
Best Local Similarity 35.4%; Pred. No. 8.9e-25;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;
OY 98 LRNMDEQQA-----SLDYLSNOVVELMNRVLLLTTEVERKQD-----PFP 139
DB 137 LKNAKQDGLGRLLETLHLYNMNNIENYVDKVANLTVV--NSLDGCSKCPSEHMQ 194
OY 140 HRPVQSHGL-DCTDIKDTIGSVTKPPSGLYIIHPESSYRPEVACMDYRGCGWTVQK 197
DB 195 SOPVQ-HLYYKDCSD-HYVLG--RRSSGAVRYVTPDHRNSFEVYCDMETMGWTVLQA 249
OY 198 RIDGIDIFORLMCDYLDGFGDGLGEMFLGKIFLYINOKNTPFMYLVALESDPTLAAV 257
DB 250 RIDGSINFTREKKDYKAGFENLREMLGDKIHLTL--KSKEMILRIDLEDPNGULTYA 307
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QY 258 SYDNFLEDETRFFKMHGRLGYSNAGDAFRGLKEDNQNAMPSTSYDNDGCRPACTVN 317
 DB 308 LVDQFYVANEFLKYLRLHIGYNTAGDADR-FSRHYNHDLRFFPTTPDRDNDRPSG---- 362
 QY 318 GQSVKSGSHLHNTGMWNEBCGLANLNG-IHHSGLKATLGOMGWTKNN--SPVAKRS 374
 DB 363 -----NCG-LIYSSGWWFDSCLSANLNGKYHOKYKGVNRGRTWPGIINQAPGGYKS 416
 QY 375 VSMKIRMYNP 385
 DB 417 SFGQAKMTRP 427

RESULT 3
 AGPL_BOVIN STANDARD; PRT; 481 AA.
 AC 018930:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensin-1 precursor (ANG-1) (Fragment).
 GN ANGPT1 or ANG1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=99054348; PubMed=9840613;
 RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
 RT "Analysis of blood vessel maturation processes during cyclic ovarian
 angiogenesis.";
 RL Lab. Invest. 78:1385-1394(1998).
 RN [2]
 RP SEQUENCE OF 91-200 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=98451564; PubMed=9776732;
 RA Mandiote S.J., Pepper M.S.;
 RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular
 endothelial cells by cytokines and hypoxia.";
 RL Circ. Res. 83:852-859(1998).
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 HEART EARLY DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
 CYCLE.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC EMBL: AF093573; AAC61872.1; -
 CC EMBL: AF032923; AAC78245.1; -
 CC HSSP: P02671; IFZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Glycoprotein; coiled coil; Signal.
 FT SIGNAL 1 15 POTENTIAL.

FT CHAIN 16 >481 ANGIOPOIETIN-1.
 FT DOMAIN 153 261 COILED COIL (POTENTIAL).
 FT FIBRINOGEN C-TERMINAL.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 481 481
 SQ SEQUENCE 481 AA; 55556 MW; 8EEC9ED84FC2BB50 CRC64;

Query Match 19.0%; Score 400.5; DB 1; Length 481;
 Best Local Similarity 27.9%; Pred. No. 2; Se-24;
 Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;

QY 23 VQNCVHSTDSVYVNIIVEGNSNAKDESKSNDYCKEDCEGSDVKRTIRREKHFCRN 82
 DB 115 IQQNAVONHT-----ATMLEIGTSLST-----AQTRKLDVETQVLANQTSREIQL 163
 QY 83 LQNSIVSY-----
 DB 164 LENSLSYKLEKQLQOQTNELIKHEKNSLLEHKIFEMEGKHKELDPTLKEKKNLQGLV 223
 QY 103 DEQASLDYLSNOYN-----ELM-----NRULLTTEV-----RKQLDPP 139
 DB 224 TRQTYIIQLELEKOLNRRATNNVLOKQOLELMDTVHMLVNLCTKEVLLKGGRKEEPF- 282
 QY 140 HRPVQSHGLDCTDKIDTIGSVTKTPSGIYIIHPGSSYPFEVMDMDYRGSGMTVIQRI 199
 DB 283 -----RQCADY-----QAGFNKSGIYIYIINMEPEKPVFCMDLNGGWTIOHRE 330
 QY 200 DGIIDFORLMDYLDGFGLLGEFLLGLKIFYIVNOKNTSFMLYVALSEDDTLAYASY 259
 DB 331 DGSIDPFGRKMEKYMKGNGSGEYWLGNFIFATTSR--QYLRILLDMEGRAASQY 388
 QY 260 DNFWLEDETRFFKMHGRLGYSNAGDAFRGLKEDN--QNAMPSTSYDNDGCRPAC--L 315
 DB 389 DRFHIGNEKONYRLYLGHGTAG-----KQSLIHGADSFSTKADADNDCMKCALM 441
 QY 316 VNGSVKSGSHLHNTGMWNEBCGLANLNGIHHS-----CKLATGIGW 360
 DB 442 LTG-----GWWFDACGSPNLNGMFTYAGNHGKL--NGIKW 475

RESULT 4
 ANL2_MOUSE STANDARD; PRT; 493 AA.
 AC Q9R045:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensin-related protein 2 precursor (Angiotensin-like 2).
 GN ANGPT2 OR ARP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=99403103; PubMed=10473614;
 RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
 Koh G.-Y.;
 RT "Molecular cloning, expression, and characterization of angiotensin-
 related protein, angiotensin-related protein induces endothelial cell
 sprouting.";
 RL J. Biol. Chem. 274:26523-26528(1999).
 CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
 AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
 SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMS
 AND TESTIS.

CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

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CC or send an email to license@sdb-sdb.ch).

CC

DR EMBL; AF125176; AAD5358.1; -

DR HSSP; P02671; 1PZD.

DR MGP; MGI:1347002; Angp12.

DR InterPro: IPR002181; Fibrinogen_C.

DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN-AG-C-DOMAIN; 1.

KW Signal; Colled coil; Glycoprotein.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 493 ANGIOPROTEIN-RELATED PROTEIN 2.

FT DOMAIN 77 115 COILED COIL (POTENTIAL).

FT DOMAIN 152 202 COILED COIL (POTENTIAL).

FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 493 AA: 57118 MW: 22855ABEF0746BF2 CRC64:

Query Match 19.0%; Score 400.5; DB 1; Length 493;

Best Local Similarity 26.7%; Pred. No. 2.6e-24;

Matches 107; Conservative 66; Mismatches 107; Indels 121; Gaps 15;

OY 68 KKIRREHFHCRLQNSIVSTSTKLLRNMDQASLDYLSNQVNEMLNRVLIT 127

DB 119 EKLRLKES---RNNNSKV---TOLYQLLHEIIRKRNAL---ELSOLENRILNQT 166

OY 128 TEVFR---KOLD-----GLDCTDIDKDTIGSVTKTPSG-----PEPIRP----- 142

DB 167 ADMQLASKYKDLKHKFOHLMLAHNOSFVIAOLEHCORVAPARMPPPRAAPRVQ 226

OY 143 -----VQSH-----GLDCTDIDKDTIGSVTKTPSG----- 166

DB 227 PTYNRRIINQISTNEIOSQNLKVLPPSLPTPALTSIPSSYDKSGSPRDCIQALEDDH 286

OY 167 ---LYIHPESSYPFEVWCMDYRGSGWTVIOKRIGIIDFORLMCYLDGFGDILGE 222

DB 287 STSSITLVKPEPTNRLMQWCDQRHDPGGWTVIOKRIGIDSVNFERKMETYKQGFNDGE 346

OY 223 FWLGLKRTFYIVNOKNTSEMLYVALESEDDTLAYASYDNFWLEDETRFFKMLGRYSNA 282

DB 347 YWLGLENITWLTNGCN--YKLLVTMEDMSGKRVAFVAFSFLPESEYKRLGLRGHNA 404

OY 283 GDAFGLKKEKNQNMAMPSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMWFNECCGAN 342

DB 405 GDSFTW---HNGKQFTTLDRDHD-----VYTG---NCAH-YQKGGWVYNACAHSN 447

OY 343 LINGIHFGSKLLA---TGIOGWTNKNNSPVKIKSVSMKIR 380

DB 448 LMGVMTRGHYSRYQDGYVAEF--RGGSYSLLKRVVMIR 486

RESULT 5

ANL2_HUMAN

ID ANL2_HUMAN STANDARD; PRT; 493 AA.

AC Q9UKU9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).

GN ANGPTL2 OR ARP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=99403103; PubMed=10473614;

RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G., Koh G.Y.;

RT "Molecular cloning, expression, and characterization of angiopoietin-related protein, angiopoietin-related protein induces endothelial cell sprouting.";

RT J. Biol. Chem. 274:26523-26528(1999).

CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN

CC AUTOCRINE AND PARACRINE ACTION.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE, SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY, ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.

CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

CC

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CC

DR EMBL; AF125175; AAD5357.1; -

DR HSSP; P02671; 1PZD.

DR GeneW; HGNC:490; ANGPTL2.

DR MIM; 605001; -

DR InterPro: IPR002181; Fibrinogen_C.

DR DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN-AG-C-DOMAIN; 1.

KW Signal; Colled coil; Glycoprotein.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 493 ANGIOPROTEIN-RELATED PROTEIN 2.

FT DOMAIN 76 115 COILED COIL (POTENTIAL).

FT DOMAIN 152 206 COILED COIL (POTENTIAL).

FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 493 AA: 57104 MW: 0F2ADECE35D185CA CRC64:

Query Match 19.0%; Score 400; DB 1; Length 493;

Best Local Similarity 31.9%; Pred. No. 2.9e-24;

Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

OY 117 NELMRVLLITEVFRKQ---LDPFPIRPVQSHGCDCTDIKDTIGSVTKTPSG----- 166

DB 231 NRIINOI--STNEIOSDQMLKVLPPPLPMPPLT-----SLPSSTDKPSGWRDC 278

OY 167 ---LYIHPESSYPFEVWCMDYRGSGWTVIOKRIGIIDFORLMCYLDGFGDILGE 222

DB 279 LQALEDHGHTSSITLVKPEPTNRLMQWCDQRHDPGGWTVIOKRIGIDSVNFERKMETYKQ 338

OY 215 GFGDLLGEFWLGLKRTFYIVNOKNTSEMLYVALESEDDTLAYASYDNFWLEDETRFFKMH 274

DB 339 GFGNIDGEXWLGLENITWLTNGCN--YKLLVTMEDMSGKRVAFVAFSFLPESEYKRL 396

OY 275 LGRTSGNAGDAFGLKKEKNQNMAMPSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMW 334

DB 397 LGRYHGNAGDSFTW---HNGKQFTTLDRDHD-----VYTG---NCAH-YQKGGW 439

OY 335 FNECCGANLNGIHHSKLLA---TGIOGWTNKNNSPVKIKSVSMKIRAMPNPY 386

DB 440 YNACAHSNLNGVMTRGHYSRYQDGYVAEF--RGGSYSLLKRVVMIRPNPTF 492

RESULT 6

FGL1_HUMAN

ID FGL1_HUMAN STANDARD; PRT; 312 AA.

AC 008830; Q960M6; Q96KW6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-
 related protein 1) (HFRP-1) (Hepasocin) (HP-041).
 GN FGL1 OR HFRP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE-93290661; PubMed-8390249;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitaajima M.,
 RT Hirohashi S.;
 RT "Molecular cloning and initial characterization of a novel
 RT fibrinogen-related gene, HFRP-1.";
 RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE-21363035; PubMed=11470158;
 RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
 RA Morimoto S., Shiohara K.;
 RT "Molecular cloning and functional expression analysis of a cDNA for
 RT human hepasocin, a liver-specific protein with hepatocyte mitogenic
 RT activity.";
 RL Biochim. Biophys. Acta 1520:45-53(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Has hepatocyte mitogenic activity.
 CC -1- SUBUNIT: Homodimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Liver-specific.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D14446; BAA03336.1; -;
 DR EMBL: D87342; BAB70690.1; -;
 DR EMBL: BC007047; AAH07047.1; -;
 DR HSSP: P02671; 1FZD.
 DR GeneW: HGNC:3695; FGL1.
 DR MIM: 605776; -;
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 312 FIBRINOGEN-LIKE PROTEIN 1.
 FT DOMAIN 78 305 FIBRINOGEN C-TERMINAL.
 FT DISULFID 26 26 INTERCHAIN (POTENTIAL).
 FT DISULFID 83 112 BY SIMILARITY.
 FT DISULFID 248 261 BY SIMILARITY.
 FT CONFLICT 15 15 I -> T (IN REF. 3).
 FT CONFLICT 69 69 N -> D (IN REF. 1).
 FT CONFLICT 72 72 I -> V (IN REF. 1).
 FT CONFLICT 105 105 P -> L (IN REF. 2).
 SO SEQUENCE 312 AA; 36391 MW; 26BC82124E660C2 CRC64;

Query Match 18.9%; Score 398; DB 1; Length 312;

Best Local Similarity 34.3%; Pred. No. 2.3e-24;
 Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;
 QY 87 IVSYRSTKRLRMMDQASLDYLSQVNEMLNRLLTTEFRRO----- 134
 DB 4 VFSFILTALTI--KRETSALDECAQEQRLAQLVETTRKQOVKIKOLLQENEV 60
 QY 135 --LDPPFRPVQSHG-----LDCTDIRTIGSVYKTPSGYIIHPESGSYPFEVCMNDY 187
 DB 61 QFLDKGDMNVIYDGSNRQYADGSEIFNDGKYL-----SGFYKIRPLQSPAFSYCCMS- 115
 QY 188 RGGGWIVYQKRIGDIDPRLMCDYLDGFGDL--GEFWLGKKIYIYNQKTSFMYL 244
 DB 116 DGGGWIVYQKRIGDIDPRLMCDYLDGFGDL--GEFWLGKKIYIYNQKTSFMYL 173
 QY 245 VALESDDTLAVASDYDPFLEDEFKRMHLGRYSNAGAFRLKKEDNO-----NAMP 299
 DB 174 IDLADFEKNSRYAQYKFKYGDENYELNIGESGAGSLAGNHPPEVQWMAHORMK 233
 QY 300 FSTSDVDNDCRPACLVNGSVKSCSHLHNTGWMFNECGLANLNGIHRSGLKLA--T 356
 DB 234 FSTWDRDHNVEGCAEDQS-----GWMFNRCHSANLNGV-YSGPYTAKTDN 281
 QY 357 GIGMGITWKNNSPYKIKSVSKIR 380
 DB 282 GIWVYTW--HGWMYSLKSVYMKIR 303
 RESULT 7
 FIBR_BOVIN STANDARD; PRT; 468 AA.
 ID FIBR_BOVIN
 AC P02676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RX [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;
 RT "The sequence of amino acids at the N-terminal end of bovine
 RT fibrinopeptide B.";
 RL Acta Chem. Scand. 17:1816-1819(1963).
 RN [2]
 RP SEQUENCE OF 5-21.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides.";
 RL Ark. Kemi 16:425-436(1960).
 RN [3]
 RP SEQUENCE OF 22-53.
 RX MEDLINE-79164394; PubMed-434821;
 RA Martinielli R.A., Ingilis A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 RT bovine fibrinogen.";
 RL Arch. Biochem. Biophys. 192:27-32(1979).
 RN [4]
 RP SEQUENCE OF 44-468 FROM N.A.
 RX MEDLINE-81199473; PubMed-626803;
 RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of a cDNA clone coding for the beta chain of bovine
 RT fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.


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CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA 6 BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EMISSION-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: V00110; CAA23444.1; -.
CC PIR: A03122; FGBOB.
CC HSSP: P02673; 1F2A.
CC InterPro: IPR002181; Fibrinogen.C.
CC DR SMART: PF00147; Fibrinogen.C; 1.
CC DR PROSITE: PS00514; FIBRINAG.C.DOMAIN; 1.
CC KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
CC PEPTIDE 1 21 FIBRINOPEPTIDE B.
CC FT CHAIN 22 468 FIBRINOGEN BETA CHAIN.
CC FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
CC FT MOD_RES 6 6 SULFATION.
CC FT SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE
CC FIBRINOPEPTIDE B).
CC FT DISULFD 72 72 INTERCHAIN (WITH ALPHA).
CC FT DISULFD 83 83 INTERCHAIN (WITH ALPHA).
CC FT DISULFD 87 87 INTERCHAIN (WITH GAMMA).
CC FT DISULFD 200 200 INTERCHAIN (WITH GAMMA).
CC FT DISULFD 204 204 INTERCHAIN (WITH ALPHA).
CC FT DISULFD 208 293 INTERCHAIN (WITH GAMMA).
CC FT DISULFD 218 247 BY SIMILARITY.
CC FT DISULFD 401 414 BY SIMILARITY.
CC FT CARBOHYD 371 371 N-LINKED (GLCNAAC. . .) (PROBABLE).
CC SEQUENCE 468 AA; 53340 MW; 2DEDA2F443AAAB37 CnC64;

Query Match 18.8%; Score 395.5; DB 1; Length 468;
Best Local Similarity 27.5%; Pred. No. 6.1e-24;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

QY 27 CVHSHSTDSVYNIYEDGSNADSKNDYVCKEDCESCDVYTKITREKHF--MCRNLQ 84
DB 72 CLHADPDLGLV-----CPTGCKLQDYLVRQERPIRKSEIDLR 108
QY 85 NSIYSTSTSK-----LRRNADQOASLDYLSNOVNELMN----- 121
DB 109 NTVSVSSTSSSTFOYITLKNMKMRONOVODNENYVNESSHLEKHQLYIDETVKNKI 168
QY 122 -----RVLLTTEVFRKLDLPP-----HAPVOSHGLDIDIDITGS 159
DB 169 PTKLAVLSIIEENLSKQKLESYSTOMEYCRPCTYTCNIPVS--GKECKIIRNEE 227
QY 160 VTKPPSGLYIHPGSSYPFEVCMCDYRGGMVYQKRIDGIIDFORLWCDYLDGFDL 219
DB 228 T-----SEMYLIQPEDSSAPRYVYCDMKTEKGMWYIQNRQGSVDFGKRWDPYKGFNI 283
QY 220 L-----GEFWLGLKFIYVQKNTSEMLYVALESEDDTLVASYDNFWLEDE 267
DB 284 ATNMGKKYCVPGFYWGNDRISQITNMGPTR--LLIEMEDMKDKVYALYEGFTVONE 341
QY 268 TRFEKMLGRYSGNAGDAF-----RGLKKEDN-----QNAPESTSYVDNDGCPALVNGQ 319
DB 342 ANKIQLSVSKIKGRAGNLLIGASQLVGENRMTTTHNSMFSYTDRODNGWYTT-----D 396
QY 320 SVKSGSHLHNTQWMFNFCGLANLNGIHFSQGL-----LATGIOMGTWTNNKSPVK 371

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DB 397 PRKQCSK-EDGGGWYNRCHANPNCRYYWGGATYTDAAKHGTDDGVYWMNH--QGSWYS 453
QY 372 IKSVMKIRMYNPF 387
DB 454 MKRMSKIR----PYF 465

RESULT 8
AGPL_HUMAN STANDARD; PRT; 498 AA.
AC Q15389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN ANGPT1 OR KIAA0003.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
RP TISSUE=Fetal Lung;
RC MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compston D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonneville P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiopoietin-1, a ligand for the Tie2 receptor, by
RT secretion-trap expression cloning."
RL Cell 87:1161-1169(1996).
[2]
RP SEQUENCE FROM N.A.
RA Ohara O., Nagase T., Kikuno R., Nomura N.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE OF 307-498 FROM N.A.
RC TISSUE=Bone marrow;
RA MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K14A0001-K14A0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1."
RL DNA Res. 1:27-35(1994).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: GLYCOSYLATED.
CC -1- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC ISCHEMIC HEART.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: U83508; AAB50557.1; -.
CC EMBL: D13628; BAA02793.2; ALT_INIT.
CC HSSP: P02671; 1F2D.
CC Genew: HGNC:484; ANGPT1.
CC MIM: 601667; -.

```

DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
 KW Glycoprotein; Coiled coil; Signal; Polymorphism.
 FT SIGNAL 1 15
 FT CHAIN 16 498
 FT DOMAIN 81 119
 FT DOMAIN 153 261
 FT DOMAIN 284 498
 FT CARBOHYD 92 92
 FT CARBOHYD 122 122
 FT CARBOHYD 154 154
 FT CARBOHYD 243 243
 FT CARBOHYD 295 295
 FT VARIANT 269 269
 FT MISSING (IN CELL LINE T98G; MAY BE DUE TO EXON SLIPPAGE).
 FT /FTID=VAR_009940.
 SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
 Query Match 18.8%; Score 395; DB 1; Length 498;
 Best Local Similarity 27.0%; Pred. No. 7,2e-24;
 Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;
 QY 23 VQNCVHSHSDSVYNIVEDGSNAKDESKSNDYCKEDCESCDYKRTITREKHFMCRN 82
 DB 115 IQQNAVONHT---ATMLEIGTSLISOT-----AEQTRKLTVEYVQLNQTSLRLQL 163
 QY 83 LQNSIVSY-----TRSTKLLRNMM 102
 DB 164 LENSLSYKLEKOLLQOTNELIKHEKNSLLEKILEMEGKHKEELDTLKEEKENLQGLV 223
 QY 103 DEQASLDYLSNOYV-----ELM-----NRVLLLTVEF-----RKQIDPF 138
 DB 224 TRQYIIQLELEKQKRNATNNVLOKQOELMDVYHNLVNCSTEGVLLKGRKEEERPF 283
 QY 139 PHRPVQSHGDCDIDKDTIGSVTKPSGLYTIHREGSSYPREVNCMDYRGSGWTYQKR 198
 DB 284 -----RDCADV-----QAGFNKSGIYIYIYNNMDEPKVPCNMDVNGCGWTYQHR 330
 QY 199 IDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFIYVQKNKSNFMYLYALBESDPTLAYAS 258
 DB 331 EDGSLDFQRGKKEYKMGFGNPSGEYWLGNERTFAITSOR--QYMLRIELMDWEGNRAYSQ 388
 QY 259 YDNFWLEDETRFEMHIGRYSGNAGDAFRGLKEDN--QNAAPRSTSDVDNDGCRPAC-- 314
 DB 389 YDRHIGNENQNYRLYLKHTGTAG-----KQSLILHGAIDSTDAADNDGCMCKCAL 441
 QY 315 LVNGQSVKSCSHLHNTGWFNNECGLANLNGIHHFS---GKLLATGIQMGSTWTKNNSPV 370
 DB 442 MLC-----GWFNFDACGPNLNGMFTYAGQNHGKL--NGIKWHYF--KGPSY 484
 QY 371 KIKSVSMKIR 380
 DB 485 SLKSTIMAIR 494
 RESULT 9
 AGPL_MOUSE STANDARD: PRT: 498 AA.
 ID AGPL_MOUSE 008336;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiopoietin-1 precursor (ANG-1).
 GN ANGPT1 OR AGPT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97134663; PubMed=8980223;

RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
 RA Ryan T.E., Bruno J., Radziejewski C., Maisonneville P.C.,
 RA Yancopoulos G.D.;
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
 RT secretion-trap expression cloning.";
 RL Cell 87:1161-1169(1996).
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT. AT E9 TO E11, IT IS
 CC ROUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
 CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED. MOST OFTEN
 CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS. IN CLOSE
 CC ASSOCIATION WITH ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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 CC -----
 CC EMBL: U83509; AAB50558.1; -;
 CC DR HSSP: P02671; IFFD.
 CC DR MGI: MGI:108448; Agpt.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
 KW Glycoprotein; Coiled coil; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT DOMAIN 81 119
 FT DOMAIN 153 261
 FT DOMAIN 284 498
 FT CARBOHYD 92 92
 FT CARBOHYD 122 122
 FT CARBOHYD 154 154
 FT CARBOHYD 243 243
 FT CARBOHYD 295 295
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 498 AA; 57505 MW; 285B4FDC260D800 CRC64;
 Query Match 18.6%; Score 391; DB 1; Length 498;
 Best Local Similarity 26.7%; Pred. No. 1.5e-23;
 Matches 115; Conservative 67; Mismatches 126; Indels 122; Gaps 16;
 QY 23 VQNCVHSHSDSVYNIVEDGSNAKDESKSNDYCKEDCESCDYKRTITREKHFMCRN 82
 DB 115 IQQNAVONHT---ATMLEIGTSLISOT-----AEQTRKLTVEYVQLNQTSLRLQL 163
 QY 83 LQNSIVSY-----TRSTKLLRNMM 102
 DB 164 LENSLSYKLEKOLLQOTNELIKHEKNSLLEKILEMEGKHKEELDTLKEEKENLQGLV 223
 QY 103 DEQASLDYLSNOYV-----ELM-----NRVLLLTVEF-----RKQIDPF 138
 DB 224 SRQYIIQLELEKQKRNATNNVLOKQOELMDVYHNLVNCSTEGVLLKGRKEEERPF 283
 QY 139 PHRPVQSHGDCDIDKDTIGSVTKPSGLYTIHREGSSYPREVNCMDYRGSGWTYQKR 198
 DB 284 -----RDCADV-----QAGFNKSGIYIYIYNNMDEPKVPCNMDVNGCGWTYQHR 330
 QY 199 IDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFIYVQKNKSNFMYLYALBESDPTLAYAS 258
 DB 331 EDGSLDFQRGKKEYKMGFGNPSGEYWLGNERTFAITSOR--QYMLRIELMDWEGNRAYSQ 388

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OY 259 YDNFWLEDETRFKMHLGRVSCNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPAC-- 314
DB 369 YDRFHIGNEKQVRLYLKCHGTAG-----KQSSLILHGADEFKADNDNCKCKAL 441
OY 315 LVNGSVSVSCSLHNTKGMWNEGCLANGLNHHF-----GCLLATGLOMGWTWKNSPV 370
DB 442 MLTG-----GWMFDCGSPNLNMGWFTAGONGHKL--NGIKMWF--KGPSY 484
OY 371 KIKSVSMKR 380
DB 485 SURSTTMAR 494

RESULT 10
AGP2_HUMAN
ID AGP2_HUMAN STANDARD: PRT: 496 AA.
AC 015123; Q9NRR7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Maisongier P.C., Surt C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Paradijewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=20309815; PubMed=10766762;
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2.";
RL J. Biol. Chem. 275:18550-18556(2000).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC REDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF004327; AAB63190.1; -
DR EMBL; AF187858; AAF6526.1; -
DR HSSP; P02671; 1FZD.
DR Genew; HGNC:485; ANGPT2.
DR MIM; 601922; -
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.

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DR PROSITE; P500514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Collod coll; Signal; Alternative splicing;
FT SIGNAL 1 16
FT CHAIN 17 496
FT DOMAIN 130 256
FT DOMAIN 280 496
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
FT VARSPLIC 97 148
SQ SEQUENCE 496 AA; 56919 MM; 5642A5847A7385C CRC64;

Query Match 18.1%; Score 381.5; DB 1; Length 496;
Best Local Similarity 26.3%; Pred. No. 8.4e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;

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DB 112 IQGNAYQNOT-----AMTIGTNLNT-----AEQTKLTDEAVQVLTOTTRLEQL 160
OY 76 -KHFQCRN-LQNSIVSYSTRSKL-----LRNMDEQQASL 109
DB 161 LEHSLSTNKLKQLLDQFSEINKLQDKNSFLKQVLAEMDKHIQLQSIKREKQDLQVLY 220
OY 110 DYLNSQVNEIMRVLLT--TEVFRQ-----LDPEHPVQSH 146
DB 221 SKQNSTIELEKRIYATATVNVNSVLOKQOHDLMETVNNLLTMNSTNSAKDPVAREQIS 280
OY 147 GDCCTDIKDFISVYKTPSGILYIHPEGSPYFEVACMDYGGWYQKRIIDGIFQ 206
DB 281 FBDCAEVRSS-----GHTNGITLTLPNPNSTEIKAYCDMEAGGGMTIIQREDSVPDQ 336
OY 207 RLMCDYLDGFGDLGEFWLGLKRIEYVQKNTSPMLVVALESEDDTLAYASDFNFWED 266
DB 337 RTWKREKVGFGNPSEYVWLGNEFVSQLTNQCR--VYLKHLKDMGNGEAYSLYEHFYLSS 394
OY 267 ERFRRKMLHGRSGNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPACILVNGSVKSSSH 326
DB 395 EELNRYRIHLKGLTGTAGKI-----SSISQPGNDFSTGTGDNKDC-----ICKCSQ 439
OY 327 LHNKGMWNEGCLANGLNHH-----FSGKLATGLOMGWTWKNSPVKIKSVSMKR 380
DB 440 MLT-GWMFDCGSPNLNMGWFTAGONGHKL--NGIKMWF--KSGYSLKATTMAR 492

RESULT 11
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ID FIBR_HUMAN STANDARD: PRT: 491 AA.
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor (Contains: Fibrinopeptide B).
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M.J., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic

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RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
 RL Biochemistry 22:3244-3250(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RL fibrinogen.";
 RL (in) Liu C.T., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
 RP LYS-478
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RL structural variants.";
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [6]
 RP SEQUENCE OF 31-491.
 RX MEDLINE=79124640; PubMed=420779;
 RA Matt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 RN [7]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogq D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [8]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Dalmont J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RL beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 RN [9]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [10]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [11]
 RP DISULFIDE BONDS.
 RX MEDLINE=77245999; PubMed=891553;
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RL disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Matt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=9333233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RL crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RL different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [17]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE=89058942; PubMed=3194892;
 RA Schmeizer C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RL structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 RN [18]
 RP VARIANT ISE.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shitakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RL replacement of B beta glycine-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 RN [19]
 RP VARIANT NAPLES.
 RX MEDLINE=92340664; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RL thrombin binding and thrombophilia. Homozygous substitution of B beta
 RL 68 Ala-->Thr.";
 RL J. Clin. Invest. 90:238-244(1992).
 RN [20]
 RP VARIANTS JUMUIDEN AND NIJMEGEN.
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens Jumiiden (B beta Arg14-->Cys) and Nijmegen (B
 RL beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RL complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [21]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RL fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RL exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE

```
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.
CC -1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CONVERTS FIBRINOPEPTIDES A AND B FROM ALPHA 6 BETA
CC CHAINS. AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPILION-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: J00129; AA52429.1; -.
CC EMBL: J00131; AA598115.1; -.
CC EMBL: J00130; AA598115.1; JOINED.
CC EMBL: J00132; AA598116.1; -.
CC EMBL: J00133; -. NOT ANNOTATED_CDS.
CC EMBL: AF388026; AA62470.1; -.
CC EMBL: X05018; CA28674.1; -.
CC EMBL: M64983; AA18024.2; -.
CC EMBL: M26877; AA52445.1; -.
CC EMBL: M26876; AA52445.1; JOINED.
CC -----
Query Match 17.8%; Score 375.5; DB 1; Length 491;
Best Local Similarity 26.6%; Pred. No. 2.5e-22;
Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;
OY 25 GNCVHSTDSVNIYVEDGSKNAKDESKNDVYCKEDCEESCVKTKITTEKHEKHMORNLQ 84
DB 93 GCGLIADPDLGLV-----CPFGCOLEALDQE-----RPIR 124
OY 85 NSI-----VSYTRSTK---KLRNMDQOASLDYLSNOVELMN----- 121
DB 125 NSVDELNNVAVESQTSSEFYWLKLDLMQKROKQVNDNENNVNVEYSSELEKHQLYID 184
OY 122 -----RVLLITTEVERKQDPP-----HPPVOSHGLDCTD 152
DB 185 ETVNSNIPNTNLRSLILENLSKIQKLESVSAQWEYCPTCTVSCNIPVVS--GRECEE 243
OY 153 IKDTIGSVTKRPSGLYIHPGSSYPFEVGMCDYRGSGWTVIQRIDITIDFORIMCDY 212
DB 244 IIRKGGET-----SEWTLIDPDSSVAFPRYRYCDMNTENGSMYIYONRQDSVDFGRKMDPY 299
OY 213 LDGFGD-----LLGEFWLGLKKIFYIVNOKNTSFMILYALVESEDITLAVASYD 260
DB 300 KQGFENVATNTDGNKYNVCGLPGEYWLGNDRKISQLTRMGPTG--LLEMEMWKGDKYKAHNG 357
OY 261 NWMLEDETFEFMHAGRYSGNAGDAFRG-----LKKEDN-----QNAPEFSTVDNDGCRP 312
DB 358 GTTYONENAKRYQISVYKRYGTAGNALMDGASOLDGEMNRTMTHNGFEFTYDRDNG--- 414
OY 313 ACTLVNGQSVKSGSHLNKNGWMEFNECGLANLNGIHFGSKL-----LALGIDMGTF 364
DB 415 --WLSDPKQCK--EDGGGMYNRCNHAANPGRYTWGQYTWMAKAGCTGDGVVMMNW- 470
OY 365 KNSPVIKISVSMKIRTRMTPYE 387
DB 471 -KGSWYSMKRSMKTR---PFF 488
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DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Angiopoietin-2 (ANG-2) (Fragment).
GN ANGP2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmula S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN [2]
RP SEQUENCE OF 219-355 FROM N.A.
RC TISSUE=adrenal cortex;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE. OVEREXPRESSED DURING LUTEOLYSIS. THIS COULD REFLECT THE
CC REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
CC THE MIDSTAGE CORPUS LUTEUM.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: AF094699; AAC62490.1; -.
CC EMBL: AF032924; AAC78285.1; -.
CC HSSP: P02671; 1F2D.
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C.1.
CC SMART: SM00146; FBG.1.
CC PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
CC KW Glycoprotein; Coiled coil.
CC NON_TER 1
CC DOMAIN 10 138
CC FT 159 375 FIBRINOGEN C-TERMINAL.
CC FT CAROHD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CAROHD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CAROHD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CAROHD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 272 272 S -> L (IN REF. 2).
CC SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;
Query Match 17.8%; Score 375; DB 1; Length 375;
Best Local Similarity 30.2%; Pred. No. 1.9e-22;
Matches 112; Conservative 57; Mismatches 136; Indels 66; Gaps 15;
OY 31 SDSSVNIYVEDGSKNAKDESKNDVYCKE--DCESCVKTKITTEKHEKHM--CNRNLNS 86
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Db	46	STNLEKQIIDLQVSEISKLODKNSFLEKKVYLWDMEDKHIIYVLRISKEKODLOVLYVSKONS	105
Qy	87	IVSTRS---TKILRMMDQOASLDYLSNOVELMR-----VILLTTE--VFRKOLD	136
Db	106	IIIELEKQIYATAVNNNSVLQKQHDIMEFVNNLLTMTSSNPYSYSLAKDEQIIFR----	161
Qy	137	PFHRPQVSHCLDCTDIKOTIGSYTK---TPSGCIYIHPGSSYPREVMCDMDYRGGGWT	193
Db	162	-----DC-----GEAFKSGLTSGYTLTFPNSSTELIAYCDMGTGGGGWT	202
Qy	194	VIOKRIGIIDFOFLMCDYLDGFDLLIGEFMLGIKFIYVONKNISFMIYVLESDDT	253
Db	203	VIOREGSVDPEQMTWEYKVFGEFNPSEGHMLGNEFVSQVTGQR--YVLIKIHRLDWEGN	260
Qy	254	LAVASYDNFMLEDETRFEFKMLHGRYSGNACDAFRLKEDNONAMPESTSDVNDGCRPA	313
Db	261	EAVSLYDHFYLSNELMYRRIHKLITGTACKI-----SSTSGQGNDSPTDADNDKC---	312
Qy	314	CLVNGOSVYKSCSHLHNTGMWFNECGLANINGIHH---FSGKILATGIOMGTWTKNSP	369
Db	313	-----ICKSQMLT--GWMWFADGCPSNLNGMYTPQROMTNKF--NGIKMYTW--KGS	360
Qy	370	VKISVSMKIR	380
Db	361	YSLKATYTMIR	371

RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A AND GAMMA-B).
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peol C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC Tissue-Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC Tissue-Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 27-437.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants."
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [7]
 RP SEQUENCE OF 75-286 FROM N.A.
 RC Tissue-liver;
 RA MEDLINE-92119334; PubMed-1685103;
 RA Marchetti L., Zaneli T., Malcovati M., Tencini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene."
 RL DNA Seq. 1:419-422(1991).
 RN [8]
 RP SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA MEDLINE-85030379; PubMed-6092346; Comeau C.M., Kant J.A.,
 RA Fornace A.J. Jr., Cummings D.E.,
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen."
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [9]
 RP SEQUENCE OF 209-270 FROM N.A.
 RA MEDLINE-84069777; PubMed-6689067;
 RA Imam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen."
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RP SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
 RA MEDLINE-82068993; PubMed-7306501;
 RA Wolfenstein-Todel C., Moessens M.W.;
 RT "Carboxy-terminal amino acid sequence of a human fibrinogen
 RT gamma-chain variant (gamma')." ;
 RL Biochemistry 20:6146-6149(1981).
 RN [11]
 RP REVIEW, AND DISULFIDE BONDS.
 RA MEDLINE-83254370; PubMed-6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen."
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.W., Doolittle L.R., Friesner S.J.;
 RT (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RP DISULFIDE BONDS.

RX MEDLINE-76225080; PubMed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen."
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE-83231465; PubMed-6860649;
 RA Hoeprich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation."
 RL Biochemistry 22:2049-2055(1983).
 RN [15]
 RP SULFATION.
 RX MEDLINE-91369960; PubMed-1892842;
 RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
 RT "Recombinant human fibrinogen and sulfation of the gamma' chain."
 RL Biochemistry 30:9414-9420(1991).
 RN [16]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE-84305751; PubMed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin."
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [17]
 RP POLYMERIZATION SITE.
 RX MEDLINE-85014892; PubMed-6592597;
 RA Horwitz B.H., Vardi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [18]
 RP POLYMERIZATION SITE.
 RX MEDLINE-81142375; PubMed-6451630;
 RA Oleksa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site."
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [19]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84203545; PubMed-6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain."
 RL Biochemistry 23:1767-1774(1984).
 RN [20]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84185664; PubMed-6325435;
 RA Plow E.F., Strouj A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets."
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [21]
 RP CALCIUM-BINDING SITE.
 RX MEDLINE-85261382; PubMed-3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by terbium fluorescence."
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [22]
 RP CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
 RX MEDLINE-81054908; PubMed-6933547;
 RA Wolfenstein-Todel C., Moessens M.W.;
 RT "Human plasma fibrinogen heterogeneity: evidence for an extended
 RT carboxyl-terminal sequence in a normal gamma chain variant
 RT (gamma')." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE-97169449; PubMed-9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., Je Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen." ;

RL Structure 5:125-138(1997).
RN [24] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RX MEDLINE=97352771; PubMed=9207064;
RA Pralt K.P., Cole H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
RT "The primary fibrin polymerization pocket: three-dimensional
structure of a 30-kDa C-terminal gamma chain fragment complexed with
the peptide Gly-Pro-Arg-Pro.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [26]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.U., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [27]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.U., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RT

Query Match 17.7%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 4,6e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

QY 85 NSIVYTRSTKRLRNMQ-----QASLDYLSNOVNELMNRVLLTTEVFRKQDPF 138
DB 103 NMIDATLTKSRKMLEIKMEYASILTHDSIRYLQETVNSNOKIVNLEKV--AQLEAQ 160
QY 139 PRRP-----VQSH---GLDCTDIKDTIGSYTKTPSGLYIIHPGSSYFEVCMQMDYRGCG 191
DB 161 COEPCKDVTVOIHDTGKDCQD---IANKAKOSGLYFIKPLKANOQFLVYCEIDSGNG 216
QY 192 WTVIQRIDGIDFORLMQDYLDFGFDL---LGEFHWGLGKKIFVYNQKNTSFMLYVAL 247
DB 217 WTVFQKRLDGSYDFKKNMVIQYKEGFGHLSPTGTTEFWLGENEKIHLISTQSAIPYALVEL 276
QY 248 ESEDDTLAYASYDNFWLEDETRFFKMHGKYS-GNAGDAFRGLKED-----NONAM 298
DB 277 EDWNGRTSTADYAMFKVGEADKYRLTYAYFAGGADAGDAFDGFDGDDPSDKFTSHNGM 336
QY 299 PFSTDVDNDGCRPACLVNGOSVSKCSHLHNTGWMFNECGLANLNGIHHSGL----- 353
DB 337 OFSTVDNDNDKFEKGCAEDGS-----GWMNKNCHAGHLNGVYYOGGTYSKAST 385
QY 354 ---LATGIOMGTWTKNNSPVKIKSVSMKI 379
DB 386 PNGYDNGIIMATW--KTRWYSMKKTTMKI 412

Search completed: December 16, 2002, 17:34:39
Job time : 10.2381 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:08 ; Search time 29.234 Seconds
(without alignments)
2732.835 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLFLNVCIFG.....PYKIKSVSMKIRMYNPFYK 388

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	427.5	20.3	652	5	09NDQ1	09ndq1 ciona lntes
2	425	20.2	491	4	095841	095841 homo sapien
3	409.5	19.5	357	11	09EPT7	09ept7 rattus norv
4	404.5	19.2	493	11	09JY03	09jy03 rattus norv
5	399.5	19.0	489	13	090218	090218 brachydanio
6	390	18.5	498	6	09BDY8	09bdy8 sus scrofa
7	383.5	18.2	308	5	09U8M6	09u8m6 tachyples
8	382	18.2	495	4	09P2Y7	09p2y7 homo sapien
9	380	18.1	346	4	043827	043827 homo sapien
10	379.5	18.0	496	11	09D2D2	09d2d2 mus muscuiu
11	378.5	18.0	316	5	0908W7	0908w7 tachyples
12	378.5	18.0	407	13	09DER1	09der1 gallus galli
13	378.5	18.0	488	13	091589	091589 xenopus laee
14	376.5	18.0	493	13	09DER2	09der2 gallus galli
15	376.5	17.9	441	13	09DER0	09der0 gallus galli
16	373.5	17.8	496	6	09BDY7	09bdy7 sus scrofa

17	369.5	17.6	220	5	08TBA2	08TBA2 clona savig
18	368.5	17.5	407	13	09PU54	09PU54 gallus gall
19	368.5	17.5	436	4	08WUR3	08WUR3 homo sapien
20	368.5	17.5	436	11	08VCM7	08VCM7 mus musculu
21	368	17.5	314	11	08WC25	08WC25 mus musculu
22	367.5	17.5	337	11	08RIQ3	08RIQ3 mus musculu
23	364.5	17.3	431	6	095LU3	095LU3 macaca fasc
24	364.5	17.3	513	13	090219	090219 brachydanto
25	364	17.3	341	5	0966W1	0966W1 halocynthia
26	362.5	17.2	435	13	093568	093568 gallus gall
27	360	17.1	356	5	095P98	095P98 halocynthia
28	359	17.1	244	4	09HBP3	09HBP3 homo sapien
29	357.5	17.0	932	13	057587	057587 brachydanto
30	352.5	16.8	592	4	095697	095697 homo sapien
31	352.5	16.8	1294	4	09UOP3	09UOP3 homo sapien
32	352	16.7	324	5	095PA0	095PA0 halocynthia
33	348	16.5	292	5	09U8W8	09U8W8 tachypieus
34	347	16.5	324	5	095EP9	095EP9 halocynthia
35	341	16.2	316	6	028529	028529 mustela put
36	339	16.1	712	4	000531	000531 homo sapien
37	339	16.1	1358	4	092752	092752 homo sapien
38	339	16.1	1358	4	015568	015568 homo sapien
39	333.5	15.9	372	5	018545	018545 biophalarl
40	333.5	15.9	385	5	095U09	095U09 biophalarl
41	332.5	15.8	337	6	09BE00	09BE00 macaca fasc
42	330	15.7	1356	11	005546	005546 rattus norv
43	327.5	15.6	235	6	028763	028763 papio cynoc
44	327.5	15.6	1353	13	000546	000546 gallus gall
45	321.5	15.3	440	5	09W291	09W291 drosophila

ALIGNMENTS

RESULT 1	ID	Q9NDQ1	PRELIMINARY	PRT	652 AA.
AC	Q9NDQ1	01-OCT-2000 (TREMURel. 15, Created)			
DT	01-OCT-2000 (TREMURel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMURel. 19, Last annotation update)				
DE	Fibrinogen-like protein.				
GN	CI-FIBRN.				
OS	Clona Intestinalis.				
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;				
OC	Phlebobranchia; Clonidae; Clona.				
OX	NCBI_TaxID=7719;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	Hotta K., Takahashi H., Asakura T., Satoh B., Takatori N., Satou Y.,				
RA	Satoh N.;				
RT	*Characterization of Brachyury downstream notochord genes in the Clona				
RT	Intestinalis embryo.*;				
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB036849; BAB00626.1; -.				
DR	HSSP; P02671; 1FZD.				
DR	InterPro; IPR002181; Fibrinogen_C.				
DR	Pfam; PF00147; fibrinogen_C; 1.				
DR	SMART; SM00186; FBG; 1.				
DR	PROSITE; PS00514; FIBRIN_AG_C-DOMAIN; 1.				
SQ	SEQUENCE 652 AA; A492BA325162F0E0 CRC64;				
Query Match	20.3%	Score 427.5;	DB 5;	Length 652;	
Best local Similarity	30.7%	Pred. No. 1e-26;			
Matches 115;	Conservative 67;	Mismatches 124;	Indels. 69;	Gaps 16;	
QY	50 SKSNDYVCK--EDCESCDYKTKITREKHFV-----CRNLQNSIVSYTR-----93				
DB	293 SQENDDAKAEADYVETVETDRTVGEVYETDETOETRTTSRQVTSRSDYVHENN 352				
QY	94 ----TKLLRNMDQOASL-----DYLNQVN--ELMNRVLLTFEVRKQL 135				
DB	353 EAMFTSTVTHAVEVTPNPYISEGSGVNIIRDYATNETGIEFTSRILRAT-----404				

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QY 136 DPFHHPVQSHGL--DCTDIDITIGSVTKTPSGLYIIHPGSSPYFVNCMDYRGSGWT 193
DB 405 NPTVQDQDQESLPYDCAEL-----ARGVQSGVYDIRP-GTKVWTVYTCMDYDGGGWT 459
QY 194 VIKRIGDIIIDFORMLCDYLDGFGDILGEFWLGLKIFYI-VNOKTSFNLVVALESDD 252
DB 460 MLOGRIDIVFSGKSKYKNGFGDINDHIGLEKMHITSKSRMELRINTLMD 519
QY 253 TLVAASDNEFWLEDETRFEKMLGRYSGNAGDARFGLKEDNOMAPSTSDVDNDGCRP 312
DB 520 VSHVANGVFIRSEGGKYLAKRYGTAGDAL-NYGENYNNHILQPTFTEDRDND----- 574
QY 313 ACIVNGSVKCSHLHNKTMGWNCGLANLNGIHFGS--KLATGIGOKGTWK----- 365
DB 575 -----GALGNCGRY--RSGWVFNAFCFANLNG--NYVGYKGVONGIYGTWYKLSGST 627
QY 366 NSPVKIKSVSMKIR 380
DB 628 SNRYSRKYVDMAKVR 642

RESULT 2
095841 PRELIMINARY: PRT: 491 AA.
ID 095841
AC 095841
DT 01-MAR-1999 (TReMBLrel. 10, Created)
DT 01-MAR-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Angiopoietin Y1 (D5595C2.2) (Angiopoietin-related protein 1 precursor).
GN D5595C2.2 OR ARPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RC MEDLINE=9148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiopoietin family
RT protein, angiopoietin-3."
RL FEBS Lett. 443:353-356(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
RA Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuko Y.,
RA Suda T.;
RT "Molecular cloning and characterization of novel angiopoietin-related
RT protein (ARPL)."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107253; AAD19608.1;
DR EMBL; AL355520; CAC13169.1;
DR EMBL; AB056476; BAB40691.1;
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal.

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FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 491 POTENTIAL.
SQ SEQUENCE 491 AA; 56719 MW; 3C4DB8DE6CF7E99 CRC64;

Query Match
Best Local Similarity 26.9%; Pred. No. 1,le-26;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDTVCKEDSCDVYKTYTRE-EKHFMCRNLONSIVSYTRSTKLLRNMM 102
DB 68 TKGQDASTIKMITHMDLENLKDYLSROKREIDYQLVVDVGNIVNEVKLLRKESRMNN 127
QY 103 DE-QQASIDYL-----SNQVLELNRYLLTFE----- 129
DB 128 SRVQLYMQLLHEIRKDNLSLESLKNNKILNVTEIMKATRYRELEVKYASLTDLVN 187
QY 130 -----VFRKQ--LDP-----FPHRPVQSHGL----- 148
DB 188 NSQVMTILLEBQCLRIFFSRQDTHVSPPLVQVPHIPNSQOYTPRGLGNETQRDPGYR 247
QY 149 DCTDIKDTIGSVTKTP-----SGLYIIHPGSSYPREV 181
DB 248 DLMPPDLATSPKSPFKIPVTFINEGPFKDCQAKBAGHSVSGIYMIKPPNSGPMQL 307
QY 182 MCDMDYRGCGWTVIQKRIDGIIDFORMLCDYLDGFGDILGEFWLGLKIFYI-VNOKTSF 241
DB 308 WCNESLDPCGWTIVIQKRIDGVSYNFFRMWENYKKGFGNIDEGWGLLENIMYSODN--Y 365
QY 242 MLYVALESDDTLVAASDNEFWLEDETRFEKMLGRYSGNAGDARFGLKEDNOMAPFS 301
DB 366 KLILIEEMSDKKVYAEVSSFRLEPSEFYLRLCTYOGNMGDSMM-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGSVKCSHLHNKTMGWNCGLANLNGIHFGSKLLA---TGI 358
DB 420 TLDRLKD-----WYAGCAHFH-KGWMYNAACASHNLNGVYGHYRSKHQOCI 468
QY 359 QMGWTWKNNSPKIKSVSMKIR 380
DB 469 FWAET--RGYSTSLNAVOMIK 488

RESULT 3
09EPT7 PRELIMINARY: PRT: 357 AA.
ID 09EPT7
AC 09EPT7
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Prothrombinase FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Rychlik D.F., Chien E., Philippe M.;
RT "FGL2 Expression in the Sprague-Dawley Rat."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF323608; AAG42269.1;
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31183DD9A02EBBA9 CRC64;

Query Match
Best Local Similarity 19.5%; Score 409.5; DB 11; Length 357;
Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;
QY 36 VVNIYEDSKNKKDESKNDYCKEDCESDV--KTKTRREKHKMKNLONSIVSYTRSR 93

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[illegible]

RESULT 4			
ID	09J03	PRELIMINARY;	PRT; 493 AA.
AC	09J03;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	Angiotensin II type 1A receptor associated protein.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=WISTAR-KYO; TISSUE=VASCULAR SMOOTH MUSCLE;		
RA	Guo D.F., Baranes D., Ono Y., Porter J.P., Abi-Jaoude E., Orlov S.N.,		
RA	Imagami T.;		
RT	"AAPI is required for recycling and resensitization of angiotensin II		
RT	type 1A receptor."		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF159049; AAF80364.1; -.		
DR	HSSP: P02671; 1FZD.		
DR	InterPro: IPR002181; Fibrinogen_C.		
DR	Pfam: PF00147; Fibrinogen_C; 1.		
DR	SMART: SM00186; FBS; 1.		
DR	PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.		
DR	Receptor.		
SO	SEQUENCE 493 AA; 57159 MW; 7C37652C472B341 CRC64;		

Query Match	19.28;	Score 404.5;	DB 11;	Length 493;
Best Local Similarity	27.18;	Pred. No. 5.5e-25;		
Matches 108;	Conservative 68;	Mismatches 118;	Indels 105;	Gaps 15;

```

0Y 62 PESDVKRKII-----REKHFMORNIQNSIVSTSTKKLLNMNDEQ--A 107
Db 125 KSRMNMNRVQVQLYQMLNHEITIRRDNALELSLENNRILNQADMLQSLSKYKDLHRKQ 184
0Y 108 STDYLSNQVNEIM-----NRVL--LTTVEFR 132
Db 165 NIDMLAHNQSEVIAQLBEHCQVRVRAARVQRPRATPRVYQRPYTKRIINQISTNEIOS 244
0Y 133 KQ---LDP-FPHRVSQHGIDCTDKDTIGSYTKTPSG-----LYII 170
Db 245 DQNLKVLPRSLPTLMAL-----SLPSIDTKRSQPMRQDQLALDEGHSTSYLV 294
0Y 171 HPGSSYFPEVMCDMDYRGGSWTVIQKRIDSIIDFQRLMCDYLDGFGDILLGEFWLGIKTI 230

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Db      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
295  K P E N T I N R L M Q W C Q O R H D P G S W T Y I Q R L D S V A F E R M W E T Y K O G F G I D E T W L G I E N I      354

Oy      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
231  F Y I V N O K T S E M L Y V A L E S E D D T L A Y A S Y D N F W L E D E T R E F K M H I G R S G N A G A F R G L K      290

Db      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
335  Y W L T N O G N - Y K L Y T M D M S G R K V A F E Y A S F R L E P E S E Y K L L G R H G A G S F W - -      410

Oy      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
291  K E D N O N A P F S T D V D N D N G C R P A C I V N G O S V K S C S H L N K T G W M F N E C G L A N L N G I H F S      350

Db      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
411  - - - - H N G K Q F T T L D R H D - - - - - Y Y T G - - - - N C A H - Y Q K G W M Y N C A H S N L N G V M Y R G      455

Oy      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
351  G K L L A - - - T G I O M G T W T K N N S P V K I K S Y M K I R R M Y N P Y      386

Db      | | : : : | | : | | | | | | | | : : | | : | | : | | : | | : | | : | | : | | : |
456  G H Y S R Y O D G Y V M A F - - R G S Y S L A K V M Y M M I R E N P T E      492

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RESULT	5
090218	
ID	090218
AC	PRELIMINARY;
DT	01-DEC-2001 (TREMBLrel, 19, Created)
DT	01-DEC-2001 (TREMBLrel, 19, Last sequence update)
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)
DE	Angiopoietin-2.
GN	ANG2.
OS	Brachydanio rerio (zebrafish) (zebra danio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI_TaxId=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=21391693; PubMed=11500985;
RA	Pham V.N., Roman B.L., Weinstein B.M.;
RT	"Isolation and expression analysis of three zebrafish angiopoietin
RT	genes.";
RL	Dev. Dyn. 221:470-474(2001).
DR	EMBL: AF379603; AAK8348.1; -.
DR	InterPro: IPR002181; Fibrinogen_C.
DR	Pfam: PF00147; fibrinogen_C.1
DR	PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; UNKNOWN.1.
QO	SEQUENCE 489 AA; 55785 MW; 3AAAE278539B33C CRC64;

Query Match	19.0%;	Score 399.5;	DB 13;	Length 489;
Best Local Similarity	28.1%;	Pred. No. 1.4e-24;		
Matches 114;	Conservative 55;	Mismatches 131;	Indels 105;	Gaps 16

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OY 23 VOGNHHSTJSSVNIIVEDSNADDEKSNJTVKEDCEESCDVTKJTRREKHFMCHN 82
Db 107 MERNVHIHOT--ATMLETGNTLLSQAEN--TCK----LTDETQVLNGTS-----R 150
OY 83 LONSTVSTRSKKLLRNMD-----EQA 107
Db 151 LEIQLEYSLSNRLKOLLEQTOEVSRLDNKSYPEOFADMEAKHSRELQAOOEKO 210
OY 108 SLDYASNQVNEJMN-----RVLLTTEVFRKODPPH-----RPyOS 145
Db 211 LLELLDRO-NELVSLLEGSLASTNSTIQLQQAOSLIDTVQOLAMATHCDISTPDK 269
OY 146 HGL---DCTDI-KDTIGSVTKTPSGLYIIHPBGSSYPEEVMQMDMDYRGGWTVIQRKD 201
Db 270 EMLKFRDCAEIPKSGV-----TENGYSIHLNPSOKIKVFCDMYTKGGGCVFQHRYPD 324
OY 202 IIDFORLMDYLDGGDGLGGEFWMGLKFTFYVYNOKNITSFMLVYALESDDTLAASYDN 261
Db 325 SYDFERNMDWYLDLGGDPBGEHMLGNDVLIHLLTTTKD--YTLQVHLKQAEHQAYSQYET 382
OY 262 FWLEEDTRFRFKMHLKRYSGSNAGDAERGLKEDNONAMPESTDVDNDCGRPACLVNGQSV 321
Db 383 FIIDEDKKYSLHANGFSTACRT-----SSLHSTQSTCDQDNDQC-----426
OY 322 KCSHSLHNKT-GWMEGECGLANGLIHNF--SGKLLATQIQMGTV 363

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Db 427 -SCKCAQMATGGMWFACGSPNLNGIYSGNSVNIYNSIKMYW 470

RESULT 6

Q9BDY8 PRELIMINARY; PRT; 498 AA.

AC Q9BDY8; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Angiopoietin 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21153163; PubMed=11230987;
RA Kim I., Moon S.O., Han G.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT "The angiotensin-II type 2 system in coronary artery endothelium prevents
oxidized low-density lipoprotein-induced apoptosis.";
RL Cardiovasc. Res. 49:872-881(2001).
DR EMBL: AF233227; AAK14992.1; -.
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00146; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 498 AA; 57413 MW; 8BC1C8EF56061876 CRC64;

Query Match 18.5%; Score 390; DB 6; Length 498;
Best Local Similarity 26.7%; Pred. No. 8.7e-24;
Matches 115; Conservative 66; Mismatches 127; Indels 122; Gaps 16;

QY 23 VQNCVNHSTDSVYVIEDGSSNANDESKSNDTVCKEDCESGVYKTKITREKHPMCRN 82
Db 115 IQQNVVNHSTDSVYVIEDGSSNANDESKSNDTVCKEDCESGVYKTKITREKHPMCRN 82
QY 83 LQNSIVSY-----ATMEIGTSLLSQT-----AEQTKILDTVETQVLYNQSRLEIQ 163
Db 164 LENSISTYKLEKQQLQQTNEILKIEKNSLBEKILIEMEGKKEELDTLKEKENLQGLV 223
QY 103 DEQASLDYLSNQVN-----ELM-----NRVLLTTEYF-----RKOLDPE 138
Db 224 TQGTIYIQLBKQRLATNNNSVLQKQLELMDYVNLNLTCTKEVYLKGGKKEEVKRF 283
QY 139 PRRVQSHGLDCTDKDTIGSVTKPPSGLYIHPREGSSYPFEVMDMDYRGSGWTVYQKR 198
Db 284 -----RDCADYV-----QAGFNKSGIYTYIYNNMPREKVFECNMDLNGGWTYIQHR 330
QY 199 IDGIIDFQRLWGLDGFGLDGEFGLGKTKFYVYNQKNTSFMLYVALESEDDTLAYAS 258
Db 331 EDGSDIDFQGMKEVYKMGFGNPSGFTWLGNEFLFALTISQ--OYTLTELMDEGNRAYSQ 388
QY 259 YDNFMLEDETFRFKMHLGRYSGNADAFGLKEDN--ONAPFSTSDVNDGCRPAC-- 314
Db 389 YDRFHLGNKQYRILYKXKHSCTAG-----KQSLILHAGDFSKDADNDNCKKCAL 441
QY 315 LVNGQSVKSCSHLHNKTKGWFNECGLANINGIHPS---GKLATGLQMGTWTKNSPV 370
Db 442 MLTG-----GWMFDACGSPNLNGMEFYTAGQNHGKTL--NGIKWHF--KGPSY 484
QY 371 KIKSVSMKIR 380
Db 485 SLRSTYTMIR 494

RESULT 7

Q9UBW6 PRELIMINARY; PRT; 308 AA.

AC Q9UBW6; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Tachylectin-5b isoform.
OS Tachyleptus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyleptus.
OX NCBI_Taxid=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398666; PubMed=10468566;
RA Gokudan S., Muta T., Tsuda R., Koort K., Kawahara T., Seki N.,
RA Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
immunity are structurally related to fibrinogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL: AB024739; BAA84190.1; -.
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00146; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 308 AA; 35136 MW; 36161E65EE77E0BF CRC64;

Query Match 18.2%; Score 383.5; DB 5; Length 308;
Best Local Similarity 29.5%; Pred. No. 1.6e-23;
Matches 114; Conservative 45; Mismatches 116; Indels 111; Gaps 15;

QY 9 LFLNVCIFIGCEVYVQNCVNH-----STDSVYVIEDGSSNANDESKSNDTVCKEDCES 64
Db 8 LFLCYSLVLVAGD-----VHNHAACSTVCSLGLIGSDYLDLDAKER----- 50
QY 65 CVKTKITREKHPMCRNLSNSTSVSTRSKTLRRMDEQASLDYLSNQVNLNRYL 124
Db 51 -----LATLQNSISCKDKAF-----YMEFTYVNTQNK-- 77
QY 125 LITTEVFRKOLDPEPRRPVQSHGL--DCTDIKDTIGSVTKPPSGLYIHPREGSSYPFEV 182
Db 78 -----AKENGLPINC-----TYVQGNRRSGIYIMPLPLNHPISVF 115
QY 183 CDMYRGSGWTVYQKRID---GIIDFQRLWGLDGFGLDGEFGLGKTKFYVYNQKNT 239
Db 116 CDMETAGGWTYVQRRGDCGQPIQNFYQWESYKNGFNLTEKFEWLGNDIIFVLNQ--D 173
QY 240 SFMLYVALESEDDTLAYASVDFNFWLEDETRFRFKMHLGRYSGNAGDAFRGLKEDNAMP 299
Db 174 SYVLRVLEDFEGRRYAEVFLVSEIELYKMSFTYKGDAGDSL-----SQHNHP 227
QY 300 FSTSDVNDGCRPACLVNGQSVKSCSHLHNKTKGWFNECGLANINGI-----HHEGKTL 354
Db 228 FTKKRDND-----KMEKNCAEAY--KGSWMYNACHSHSNLNGMYLRGPHES----- 272
QY 355 ATGIQMGTVTKNSPVKIKSVSMKIR 380
Db 273 AVGVNMYQWRGHVSLKVS--EWMKIR 296

RESULT 8

Q9P2Y7 PRELIMINARY; PRT; 495 AA.

AC Q9P2Y7; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Angiopoietin-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homalidae; Homo.
OX NCBI_Taxid=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99126459; PubMed=9927494;
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA Wands J.R.;
RT "Biologic significance of angiopoietin-2 expression in human

RT hepatocellular carcinoma."
 RL J. Clin. Invest. 103:341-345(1999).
 DR EMBL: AB009865; BAA95590.1; -
 DR HSSP: P02671; IPIZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FIB; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
 SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08P6 CRC64;

Query Match 18.2%; Score 382; DB 4; Length 495;
 Best Local Similarity 26.4%; Pred. No. 3.9e-23;
 Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

QY 23 VQGNCHSTDSVYNIIVEDGNSNADESKSNDYVCKEDCEESCDYKTKT---TREE--- 75
 DB 112 IQQAAVGNQF---AVMIEIGTNLNNQF-----AQGTRLTVEVAQVNLQTRLEQL 160
 QY 76 -KHEMCN-IONSVSTRSTKTL-----LNMMDEQOASL 109
 DB 161 LEHSLSTNKLKQILQDOTSEINKLQDRNSPLEKKVLAEMDKHIIQLQSIKEEKDQLQVLY 220
 QY 110 DYLSNOYNEIMNRYLLT--TEVPRKQ-----LDPRHPRVQSHG 147
 DB 221 SKONSTIELEKKIVTATVNNSTVLQKQOHLMETVNNLLTMSTSNKDPYVAKEQISF 280
 QY 148 LDCTDINDIGSVTKPTSGYLIHPEGSSYPFEVYCDMDYKGGGTVYQKRIDGIIIDFOR 207
 DB 281 RDCAEVEFKS---GHTNGIYTLTFPNSTEIKAYCDMEAGGGMTIIQREDESDVPR 336
 QY 208 LMCYLDGFQDLGEFNLGLKITYIVNOKNTSPMLYVALESDDTLAYASYNFWEDE 267
 DB 337 TWKEYKGFGEFNPSEYVGNFVSQLTNOQR--YVLKIHLMDEGNEAYSLYEHFYLSSE 394
 QY 268 TRFKMLIGRYSNAGAFNGLKEDNONAMPSTSDVNDGCRPACLYNQSVKSCSHL 327
 DB 395 ELNRIHLKGLTGAGKI-----SSISOPGNDSTFKGDNDKC-----ICKCSOM 439
 QY 328 HNKGTWPFNEGGLANGLNHIH---FSGKLATGIOMGTWTKNNSPVKIKSVSKIR 380
 DB 440 LT-GGMWFDACGPNLGNOMYYPQRONTNKF--NGIKMYW--KSGYSLKATYTMIR 491

RESULT 9
 ID 043827 PRELIMINARY; PRT; 346 AA.
 AC 043827;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CDP6 (Angiopoietin-like factor) (CDP6 protein).
 GN D1647M16.1 OR CDP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RC SEQUENCE FROM N.A.
 RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN 12
 RC SEQUENCE FROM N.A.
 RA Baguley C.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN 13
 RC SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN 14
 RC SEQUENCE FROM N.A.
 RA MEDLINE=21318995; PubMed=11426320;

RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
 RA Vorup-Jensen T., Thiel S., Friedl H., Hankeln T., Hall R., Gregory S.,
 RA Fujita T., Schwaible W.;
 RT "The human gene for mannin-binding lectin-associated serine protease-2
 RT (MASP-2), the effector component of the lectin route of complement
 RT activation, is part of a tightly linked gene cluster on chromosome
 RT 1p36.2-3."
 RL Genes Immun. 2:119-127(2001).
 DR EMBL: Y16132; CAAT6078.1; -
 DR EMBL: AL049653; CAB44734.1; -
 DR EMBL: BC001881; AAH01881.1; -
 DR EMBL: AJ300188; CAC15571.1; -
 DR HSSP: P02671; IPIZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FIB; 1.
 SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 18.1%; Score 380; DB 4; Length 346;
 Best Local Similarity 27.9%; Pred. No. 3.6e-23;
 Matches 107; Conservative 67; Mismatches 138; Indels 72; Gaps 15;

QY 14 VCITIGEVYQNCVHSTDSVYNIIVEDGNSNADESKSNDYVCKEDCEESCDYKTKT- 72
 DB 12 LCIFIVAFV-----SHPAWLKLSKHKTPAPQPLKAAN--C--CEEVKEIKAAVAN 58
 QY 73 -----BEKHEMCN-IONSVSTRSTKTLRNMMDEQOASLDYLSNOYNEIMN 122
 DB 59 LSLSLSELNKGQEDWVSVMQ---VMELENSKRMEKRLTDASKSEMMNQDIDMQL 115
 QY 123 VLLITTEVFRKQDLFPHPRPVQSHGLDCTDIRD--TIGSVTKPTSGYLIHPEGSSYPF 179
 DB 116 AAQVYVQTSADAI-----YDCSSLYOKNRYRISGYKLPDPDFLSPF-----L 158
 QY 180 EVMCDMDYKGGGTVYQKRIDGIIIDFORLNCDDYLDGPEFDLGEFNLGLKITYIVNOKNT 239
 DB 159 EVFCDMETSGGGWTVIIQKRSGLVSFYDMWQYKRGFGSISGDWLGHEHJHRISROPT- 217
 QY 240 SFMLYVALESDDTLAYASYNFWEDETRPFKMLIGRYSNAG--DAFRGLKEDNONAM 298
 DB 218 --RLRVEKEDMEGNIRAYEYSHFVYGNLNSYRLEFLGTYGNGDALQ-----YHNNT 269
 QY 299 PFSTSDVNDGCRPACLYNQSVKSCSHLHNTGWMFNEGGLANGLIHPSGK--LLAT 356
 DB 270 AFSTRKDKNDNC-----LDKCAQL--RKGGYWCCTDSNLNGYTYRLGEHNKHL 318
 QY 357 GICMGTWTKNNSPVKIKSVSKIR 380
 DB 319 GITWYGV--HGSTYSLKRVEMKIR 340

RESULT 10
 ID 09D2D2 PRELIMINARY; PRT; 496 AA.
 AC 09D2D2;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
 DE enriched library, clone:5031400E18, full insert sequence (Angiopoietin
 DE 2).
 GN AGPT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RC SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pletschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenlinich S., Hill D., Holmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RP [2]
RA SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019860; BAB1887.1; -
DR EMBL; BC027216; AAH27216.1; -
DR HSSP; P02671; 1FZD.
DR MGD; MGI:1202890; Agp12.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;

Query Match 18.0%; Score 379.5; DB 11; Length 496;
Best Local Similarity 25.7%; Pred. No. 6.3e-23;
Matches 111; Conservative 71; Mismatches 125; Indels 16; Gaps 16;

QY 23 VQGNCHSTDSVYNIEDGSSNAKDESKNDYCKEDCEESCDYKTKTRREKHFMCN 82
DB 112 IQGNVYVQNT---AVMEIGTSLNQTA-----QTRKLTVEAQVQLNTTRLEQL 160
QY 83 LQNSIVSTRSTKLLRNMDQASLDYLSNQVNEMLNRYLLTTEVF----- 131
DB 161 LQHSI---STNKLEKQILDQ-----TSEINKLNKNSFLBQKVLDMGKHSQQL 207
QY 132 -----RKQ-----LQFPHRPV-----QSHGLDCTDIDKDTIGSVTK-- 162
DB 208 SMKEQKDELQVLYVSKSSYIDLEKLLVATVYNSNLLQKQH-----DLMETVNSLLTMM 262
QY 163 -----TPSGLYIHPGESSYPFPEWCMQMDYRGGM 192
DB 263 SSPNSKSVATRKERQTFRCDAELFKSGULTSGIYTLTFPSTBEIKAYCDMDYGGGM 322
QY 193 TVIQRRIGIIDFQRLKCDYLDGFGDLLGEFVLGLKKIFYIVNQNTSEMLYVALESED 252
DB 323 TVIQHREGSDVDFQRTWKREKGFSGPLGEYVLGNFVSQLTGQHR--YVLKIQLKDMEG 380
QY 253 TLAVSYDNFMEDFTREFKMLGRYSGNAGDAFRGLKKEDNQNMPPSTSDVNDGCRP 312
DB 361 NEAHSLYDHFYIAGESENRIHLTGLTGAGKI-----SSISQPSGSDSTKDSNDKC-- 433
QY 313 ACLVNGSVKSCSHLNKTKGWMFNECGLANLNGIH-----FSGKLLANGICQMGTYTKNS 368
DB 434 -----ICKCSQMLS-GGMWFADACPSNLNGOYYPOKQNNKPF--NQIKRYYM--KGS 480
QY 369 PVKIKSVSMKIR 380
DB 481 GYSLKATMTMIR 492

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE Tachylectin-5b.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398666; PubMed=10468566;
RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
RA Mizuno Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
RT immunity are structurally related to fibrinogen";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL; AB024738; BAA84189.1; -
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 316 AA; 36112 MW; 6FFBFD4159EDFID CRC64;

Query Match 18.0%; Score 378.5; DB 5; Length 316;
Best Local Similarity 29.3%; Pred. No. 4.2e-23;
Matches 113; Conservative 45; Mismatches 117; Indels 11; Gaps 15;

QY 9 LFLNCFIFICEVYVQNCVNH-----STDSSVYNIEDGSSNAKDESKNDYCKEDCEES 64
DB 16 LSLFLCYSLLVAD-----VHHHAACSTVCSLKGILDSVLDLAKER----- 58
QY 65 CVYKTRITEEKHFMCNQNLSIVSTRSTKLLRNMDQASLDYLSNQVNEMLNRYL 124
DB 59 -----LATLQNPICSKDAF-----YMETYTNVQNK-- 85
QY 125 LITTEVFRQLDPPHAPVQSHGL--DCTDIDTIGSVTKPSGLYIHPGESSYPFEM 182
DB 86 -----AEKNGLPINCA-----TYQGNKRTSGIYTLFPLNHPISVF 123
QY 183 CMDYRGGMVYIQRID--GIIDFQRLKCDYLDGFGDLLGEFVLGLKKIFYIVNQNT 239
DB 124 CMETAGAGGMVYIQRRGDCQPIQNFQWESYKNGFNLTFEPVLGNDIIVLNQ--D 181
QY 240 SFMLYVALESEDITLAYSVDNFWLEDETRFKMLGRYSNAGDAFRGLKKEDNQNM 299
DB 182 SVYLRLDLEDFGGRYAVAVFIVRSEIELYKMSFKYKGDAGDSL-----SOHNNMP 235
QY 300 FSTSDVNDGCRPACLVNGSVKSCSHLNKTKGWMFNECGLANLNGI-----HHSGLK 354
DB 236 FTTKDRND-----KWEKNCAEAY-KGGMVYNCHSNLNGMYLRGPHEES---- 280
QY 355 ATGIQMGTYTKNSPVKIKSVSMKIR 380
DB 281 AVGVMMYQWRGHNYSLKVS--EMKIR 304

RESULT 11
ID Q908W7 PRELIMINARY; PRT; 316 AA.
AC Q908W7;
DT 01-MAY-2000 (Tremblrel. 13, Created)

RESULT 12
ID Q9DER1 PRELIMINARY; PRT; 407 AA.
AC Q9DER1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Angiopoietin-2b.
GN ANGIOPOIETIN-2B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;

RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
 RA Villagrasa X., Mezquita C.;
 RT "Genomic structure and alternative splicing of chicken angiopoietin-
 2.";
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL: AJ289778; CAC08175.1; -.
 DR HSSP: P02671; 1FZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FRG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 407 AA; 46687 MW; 8663BA0AB8C7A41C CRC64;

Query Match 18.0%; Score 378.5; DB 13; Length 407;
 Best Local Similarity 26.4%; Pred. No. 5.9e-23;
 Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

QY 23 VGGNCVHHSSTSSVNVNIVEGSSNAKDESKSDNYCKEDCESGCVKRTITEEHKFMGRN 82
 DB 23 IQGTAVONOT---AVMIEGTNLNLT-----AEQTRKLTVEAQLNQTRELQL 71
 QY 83 LQNSIVSTSTSKLLR-----NMDEQASLDYLSQVNL----- 119
 DB 72 LEHSL-----STNKLEROISVQTEITKLOEKNFLEKRVLEMEDKHTLOLSIKDEKQ 126
 QY 120 -----MNRVL-----LTTEVFRKQDPPHPRVQS-HGL----- 148
 DB 127 LQVLVAHONSTIELEKQLVATVAVNSVYLQKQHDLMETVHNLMTISTPSAKKNFLAK 186
 QY 149 -----DCID-IDDTIGSYTKTPSGLYIHPGSSYFPEVMCMQMDRGGWYIYQKRID 200
 DB 187 EEOISFDCAEAFKSGI-----TTSGLYTLTFPNSAQEKRAVYCMESNGGWTYLOQRD 241
 QY 201 GIIDFQRLMCDYLDGFGLDGEFWGLKPIFYIVNOKTSPMLVVALESDDTLAYASYD 260
 DB 242 GSYDFHTWKEKIGFEDPAGETWLGNEFVSQLTNOKR--YVLKIIILKDMEGNAIYIYD 299
 QY 261 NFWLEDFREFKMHGIRYSGNAGDAFRGLKEDNQNMAMPSTSDVNDGCRPAQLVNGQS 320
 DB 300 QFYLANEOKYRIHLKLTGTAGKI-----SSISQPCNDFSTKADNDKC----- 344
 QY 321 VKSSHLNHTGWMENSCGLANLNGIHH---FSGKLLANGIOWGTYTKNNSPKIKSVS 376
 DB 345 ICKSSQMLT-GGWMEDACGSGNLGMYTPLRQNNKTF--NGIKWYV--KSGYSLKATY 399
 QY 377 MKIR 380
 DB 400 MMIR 403

RESULT 13
 Q91589 PRELIMINARY; PRT; 488 AA.
 ID 091589
 AC 091589: 091546:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Fibrinogen B-beta subunit precursor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=95369693; PubMed=7642099;
 RA Roberts L.R., Nichols L.A., Holland L.J.;
 RT "cDNA and amino-acid sequences and organization of the gene encoding
 the B beta subunit of fibrinogen from Xenopus laevis.";
 RL Gene 160:223-228(1995).
 RN [2]
 RP SEQUENCE OF 1-25 FROM N.A.

RX MEDLINE=94032285; PubMed=8218230;
 RA Roberts L.R., Nichols L.A., Holland L.J.;
 RT "Transcriptional regulation of the Xenopus laevis B beta fibrinogen
 RT subunit gene by glucocorticoids and hepatocyte nuclear factor 1:
 RT analysis by transfection into primary liver cells.";
 RL Biochemistry 32:11627-11637(1993).
 RN [3]
 RP SEQUENCE OF 1-25 FROM N.A.
 RA Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U19618; AAA85283.1; -.
 DR EMBL: U05035; AAA60463.1; -.
 DR HSSP: P02675; 1FZG.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FRG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW signal.
 FT SIGNAL 1 16
 FT CHAIN 17 43 B FIBRINOPEPTIDE.
 FT CHAIN 17 488 FIBRINOGEN B-BETA SUBUNIT.
 SQ SEQUENCE 488 AA; 54803 MW; 660E03844B6C414 CRC64;

Query Match 18.0%; Score 378.5; DB 13; Length 488;
 Best Local Similarity 28.6%; Pred. No. 7.5e-23;
 Matches 115; Conservative 49; Mismatches 143; Indels 95; Gaps 15;

QY 61 CEESGDVTKTRREKHF-----MCRNLQNSIVSTSTSKLLRNMDDEQOASLDY 111
 DB 106 CPTGCELTKTLKORNRVKTAINDRGRVETLAOSANNVYTYVGLGKIENQOQTLDN 165
 QY 112 LSNQVNL-----MNRVLLTTEVFRKQDPPHPR----- 141
 DB 166 -QNVVNEVNELEBQYTFIKNDTKIPSNRILRLQVLENRSKIQKLETAIATOVENC 224
 QY 142 -----PQSHGLDCTDKITIGSYTKTPSGLYIHPGSSYFPEVMCMQMDRGGW 192
 DB 225 SPCTYTPPIPVVS-GKEEEIYRRGGET-----SEWYLIQDPSFPRFVYCDMAITHG 279
 QY 193 TVICKRIDGIIDFQRLMCDYLDGFG-----DLGGEFWGLKPIFYIVNOKNFS 241
 DB 280 TVIONRQDGSVGFRTWDSYSGFNLANGGKICDMPGEFWGNETISQLTNIGATEA 339
 QY 242 MLYVALESDDTLAYASYDNFWLEDFREFKMHGIRYSGNAGDAFRG---LKKEDN--- 294
 DB 340 LF--EMEDWDGAKYTAQYTGFTVQNEANKYOLSVGYKTAGNMLMOSASLKGENRMT 397
 QY 295 -QNMAMPSTSDVNDGCRPAQLVNGQSVKSHLHNTGWFNECGLANLNGIHFGSKL 353
 DB 398 IHNGMFSTFDNDNGWQ-----HSDPNKQCSK-EDGGGWMYNRCHAMPNGRYWGGY 451
 QY 354 -----LATGIOWGTYTKNNSPKIKSVSMKIRMYNPEY 387
 DB 452 TWDMAKHGTDDGVVWMMN--KDSWYSMKKMSIKIR---PYF 487

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 ID 09DER2
 AC 09DER2:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Angiopoietin-2.
 GN ANGIOPOIETIN-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; PubMed=10964717;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:33:13 ; Search time 12.3175 Seconds

(Without alignments)
926.822 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASILLFLNVCIFIG.....PVKIKSVSMKIRRMYPYR 388Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425	20.2	491	2	US-08-933-821-4
2	425	20.2	491	3	US-08-960-507-4
3	425	20.2	491	4	US-09-136-828-4
4	425	20.2	491	4	US-09-332-928A-4
5	425	20.2	491	4	US-09-136-801-4
6	425	20.2	491	4	US-09-332-929-4
7	413.5	19.7	439	4	US-09-442-143A-2
8	405.5	19.3	432	4	US-09-442-143A-4
9	405.5	19.3	430	4	US-08-740-223A-12
10	405.5	19.3	430	4	US-09-709-188-12
11	403.5	19.2	497	4	US-08-740-223A-4
12	403.5	19.2	497	4	US-09-709-188-4
13	402.5	19.1	497	1	US-08-373-579-4
14	402.5	19.1	497	2	US-08-418-595-4
15	402.5	19.1	497	2	US-08-665-926-4
16	402.5	19.1	497	2	US-08-348-492-4
17	402.5	19.1	497	2	US-09-162-437-4
18	402.5	19.1	497	4	US-08-817-318-4
19	400	19.0	493	4	US-08-933-821-2
20	400	19.0	493	3	US-08-960-507-2
21	400	19.0	493	4	US-09-136-828-2
22	400	19.0	493	4	US-09-332-928A-2
23	400	19.0	493	4	US-09-136-801-2
24	399	19.0	432	1	US-08-525-505A-4
25	395.5	18.8	496	4	US-08-740-223A-22
26	395.5	18.8	496	4	US-09-709-188-22
27	395.5	18.8	496	4	US-09-709-188-22

28	395	18.8	478	4	US-08-740-223A-7	Sequence 7, Appl
29	395	18.8	478	4	US-09-709-188-7	Sequence 7, Appl
30	395	18.8	495	4	US-08-740-223A-26	Sequence 26, Appl
31	395	18.8	495	4	US-09-709-188-26	Sequence 26, Appl
32	395	18.8	498	4	US-08-740-223A-2	Sequence 2, Appl
33	395	18.8	498	4	US-09-351-457-2	Sequence 2, Appl
34	395	18.8	498	4	US-09-561-500-2	Sequence 2, Appl
35	395	18.8	498	4	US-09-561-108-2	Sequence 2, Appl
36	395	18.8	498	4	US-09-351-543-2	Sequence 2, Appl
37	395	18.8	498	4	US-09-561-526-2	Sequence 2, Appl
38	395	18.8	498	4	US-09-202-491-5	Sequence 5, Appl
39	395	18.8	498	4	US-09-709-188-2	Sequence 2, Appl
40	394	18.7	495	4	US-09-351-457-5	Sequence 5, Appl
41	394	18.7	495	4	US-09-561-500-5	Sequence 5, Appl
42	394	18.7	495	4	US-09-561-108-5	Sequence 5, Appl
43	394	18.7	495	4	US-09-351-543-5	Sequence 5, Appl
44	394	18.7	495	4	US-09-561-526-5	Sequence 5, Appl
45	393	18.7	491	4	US-08-740-223A-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: The Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-933-821-4

Query Match 20.2%; Score 425; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNADESKNDYCKEDCESQVTKITRE-EKHFMCRLNDSIVSYSTRKILRNMM 102
   :||| : : :||| : : :||| : : :||| : : :|||
Db 68 TKGDASTIKMTIRMDLENKDVLSRQKREIDVLGVVDVGNIVNEVKILRESRNM 127
   :||| : : :||| : : :||| : : :||| : : :|||
QY 103 DE-QQASIDYL-----SNQVNEMLNRVLLTTF----- 129
   :||| : : :||| : : :||| : : :||| : : :|||
Db 128 SRVQLVQQLLHEIRKRDNSIELSLQENKILNVTTLEMLKMATRYRELEVYASITDLVN 187
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QY 130 -----VERKO---LDP-----PPHPRVOSHGL----- 148
Db 188 NOSVMTLLEEOCLRFESKODTHVSPPLVQVVPQHITPNSOQYTPGLLGNENIORDCYPR 247
QY 149 DCTDIKDTIGSVTKTP-----SGLYIIHPEGSSYPFEV 181
Db 248 DLMPPEDLATSPKSPFKIPRYTFINEGPFKDCQAKKAGHSVSGIYMIKPEKNSGPMOL 307
QY 182 MCDMDYRGGMWYIQRKIDGIIDFORLWCDYLDGFEDLLGEFPLGKIKFYIYNQNTSEF 241
Db 308 WCNESLDPGGMWYIQRKIDGVSVEFFRNWENYKKGFGNIDGEXWLGIENIYMLNSQDN--Y 365
QY 242 MLYVALESEDDPLAYASYNFMLEDETREFKMHIGRYSNAGAPFGLKKEKNQNMPS 301
Db 366 KLIIELEDMSDKRYVAEYSFRLPESEFYLRLGLTYQGNAGDSMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWFNECGLANLNGIHFGSKLLA---TG1 358
Db 420 TIDRDKD-----MYAGNCAHFH-KGGMWYNACAHSNLNGVYRGHTRSKHQDGI 468
QY 359 QMGWTNKNNSPVKIKSVSKIR 380
Db 469 FWAEX--RGGSYSLRAVQMMIK 488

RESULT 2
US-08-960-507-4
; Sequence 4, Application US/08960507
; Patent No. 6057435

; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregier, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-960-507-4

Query Match 20.2%; Score 425; DB 3; Length 491;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDTVCKEDCESCDVYKTKITRE-EKHFMCRNLONSIVSYRSTKLLRNMM 102
Db 68 TGGQASATIKQWITMDLENLKDVLRSROKRELDIVLQLVVDVGNGIVNEVKLLRKESRMMN 127

QY 103 DE-QQASLDYL-----SNOVNELMNRVLLITTE----- 129
Db 128 SRVTOYLMOLLEIRKRDNSLELSOLENKILNVTTMLKMATRYRELEVKYASLTDLVN 187
QY 130 -----VERKO---LDP-----PPHPRVOSHGL----- 148
Db 188 NOSVMTLLEEOCLRFESKODTHVSPPLVQVVPQHITPNSOQYTPGLLGNENIORDCYPR 247
QY 149 DCTDIKDTIGSVTKTP-----SGLYIIHPEGSSYPFEV 181
Db 248 DLMPPEDLATSPKSPFKIPRYTFINEGPFKDCQAKKAGHSVSGIYMIKPEKNSGPMOL 307
QY 182 MCDMDYRGGMWYIQRKIDGIIDFORLWCDYLDGFEDLLGEFPLGKIKFYIYNQNTSEF 241
Db 308 WCNESLDPGGMWYIQRKIDGVSVEFFRNWENYKKGFGNIDGEXWLGIENIYMLNSQDN--Y 365
QY 242 MLYVALESEDDPLAYASYNFMLEDETREFKMHIGRYSNAGAPFGLKKEKNQNMPS 301
Db 366 KLIIELEDMSDKRYVAEYSFRLPESEFYLRLGLTYQGNAGDSMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWFNECGLANLNGIHFGSKLLA---TG1 358
Db 420 TIDRDKD-----MYAGNCAHFH-KGGMWYNACAHSNLNGVYRGHTRSKHQDGI 468
QY 359 QMGWTNKNNSPVKIKSVSKIR 380
Db 469 FWAEX--RGGSYSLRAVQMMIK 488

RESULT 3
US-09-136-828-4
; Sequence 4, Application US/09136828
; Patent No. 6350450

; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,828
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregier, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130R1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-136-828-4

Query Match 20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDTVCKEDCESCDVYKTKITRE-EKHFMCRNLONSIVSYRSTKLLRNMM 102

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Qy      130 -----VFRKO---LDP-----FPHRPVOSHGL-----148
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Qy      149 DCDIDIKDTIGSVTKTP-----SGLYIHPBGSSYTFEV 181
Db      248 DLMPPPLATSPKSPKIPPVTFINEGPRKDCQQAKEAGHSVSGIYMIKRPENSNGMOL 307
Qy      182 MCDMDYRGGWTVYQKRIIDGIIDFORLMCDYLDGFDLLGEFNLGKIFYIYVOKTSTF 241
Db      308 WCNNSLDPPGWTYQKRTDSVNFRRMWNKKGFGINDSEYWLGLENITMLSNQDN--Y 365
Qy      242 MLVVALESEDDTLAYASYDNFWLEDETRFFKMLGRYSGNAGDAFRGLKREDNONAMPFS 301
Db      366 KLIELEDMSDKRYVAEYSSFRLEPESEFYRLRLGTGYQGNAGDSMMV-----HNGKQFT 419
Qy      302 TSDVNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFGSKLLA---TGI 358
Db      420 TLDKDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy      359 QMGWTWKNNSPVKIKSYMKIR 380
Db      469 FMAEY--RGGSYSILRAVQMMIK 488

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RESULT 4
US-09-332-928A-4
Sequence 4, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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US-09-332-928A-4
Query Match      20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1,3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

Qy      44  SNKDESKNDYCKECCESCQVYKTYRRE-EKHFCRNLQNSIVYSTSKLLRNMM 102
Db      68  TKGQDASTIKDMITRMDELNKLVDLSROKREIDVQLVVDGNIYEVKLLRKESHNM 127
Qy      103 DE-QQASLDYL-----SNOVNEIMNRVLLITTE-----129
Db      128 SRVQLYMLLHETIRKRONSLLELSQLENKILVNTTEMLKATRYRELKVKASLIDLVN 167
Qy      130 -----VFRKO---LDP-----FPHRPVOSHGL-----148
Db      188 NOSVMITLLEEQCLRIETSRQDTHVSPPYQVVPQHIFPNSQOYTPGLGNEIORDPGYPR 247
Qy      149 DCDIDIKDTIGSVTKTP-----SGLYIHPBGSSYTFEV 181
Db      248 DLMPPPLATSPKSPKIPPVTFINEGPRKDCQQAKEAGHSVSGIYMIKRPENSNGMOL 307
Qy      182 MCDMDYRGGWTVYQKRIIDGIIDFORLMCDYLDGFDLLGEFNLGKIFYIYVOKTSTF 241
Db      308 WCNNSLDPPGWTYQKRTDSVNFRRMWNKKGFGINDSEYWLGLENITMLSNQDN--Y 365
Qy      242 MLVVALESEDDTLAYASYDNFWLEDETRFFKMLGRYSGNAGDAFRGLKREDNONAMPFS 301
Db      366 KLIELEDMSDKRYVAEYSSFRLEPESEFYRLRLGTGYQGNAGDSMMV-----HNGKQFT 419
Qy      302 TSDVNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFGSKLLA---TGI 358
Db      420 TLDKDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy      359 QMGWTWKNNSPVKIKSYMKIR 380
Db      469 FMAEY--RGGSYSILRAVQMMIK 488

```

RESULT 5

US-09-136-801-4
Sequence 4, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.


```

; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fg12
US-09-442-143A-2

Query Match
Best Local Similarity 19.3%; Score 413.5; DB 4; Length 439;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 34 SSVNIYEDGSKNAKDESKSDTYCKEDCE-----ESCQVTK 70
D 73 SRIEVEKQVNLKEIYNSLKKSC-QDCKLOADNGDPGRGLLPSTGAPGEVDNRV 131
QY 71 ITREKHEKCRNLONS---IVSYTRSTKRLRNM-----MDQOASLDYLSNQVLELM 120
D 132 ELSEVYKLSSELKNAKEEINVLHGRLKELNLYMNNIENYVDSKANLFFVNSLDGKC 191
QY 121 NRVLITTEFRKQLODFPHRPQVSHL--DCTDIKDTIGSVYKTPSGLYIIEGSSYP 178
D 192 SKC-----PSQEQIGSRPVO-HLIVKDCSDY---AIGRSSEYTRVPDPKNS 237
QY 179 FEVACDMHYGGGWTVYOKRIDGIIDFQRLMCDYLDGFDLGEFWMGLKFIYVQKN 238
D 238 FEVYCMETGCGGTIVYQARLDGSTNTRWQDYKAGFNLRREFWLGNDKIHLTF--KS 295
QY 239 TSFMYLVALESEDDTLAASYDNFMLEDETRFEKMLGRYSGNADAFRLKKEDNONAM 298
D 296 KEMILRIDLEDENGVELYALYDQYVANEFLKRYLHYGNTGADALR-FNKHYNDLK 354
QY 299 PFSISVDNDCRPACLYNQSQVSKSHLNKGTGWFNEGCLANLG-IHFFSGKLATG 357
D 355 FETTPDKNDNRYPSG-----NCG-LYSSGWFDPACLSANLNGKYYHQKRYGVRNG 404
QY 358 IONGTW--TKNSPVKIKSYSMKIRMYNP-YFK 388
D 405 IFWGTWPGVSEARHGKYSSEKAKMMIRKHKR 438

RESULT 8
US-09-442-143A-4
; Sequence 4; Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fg12
US-09-442-143A-4

Query Match
Best Local Similarity 19.3%; Score 405.5; DB 4; Length 432;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LRNMMDQQA-----SIDYLSNOVNELMNRVLLITTEFRKOLD-----PPF 139
D 137 LKNAKDDIOGQGRLETLHLVNMNNIENYVDSKANLFFVNSLDGKCSCPSOEHMQ 194
QY 140 HRPQVSHL--DCTDIKDTIGSVYKTPSGLYIIEGSSYPFEVACDMHYGGGWTVYOK 197
D 195 SQRYVQ-HLIVKDCSD-HYVIG---RSSGAYRVPDPKNSFEVYCMETGCGGTIVYQAR 249
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QY 198 RIDGIIDFQRLMCDYLDGFDLGEFWMGLKFIYVQKNKTSFMYLVALESEDDTLAYA 257
D 250 RLDGSTNTRWQDYKAGFNLRREFWLGNDKIHLTF--KSKEMLRIDLEDENGVELYAL 307
QY 258 SYDNFMLEDETRFEKMLGRYSGNADAFRLKKEDNONAMPEFSTVDNDCRPACLYN 317
D 308 LYDQYVANEFLKRYLHYGNTGADALR-FSRHYNDLREFFTVPDNDNRYPSG---- 362
QY 318 GQVSKCSHLNKGWFMNEGCLANLG-IHFFSGKLATGIOMGTWTKN--SPVKRS 374
D 363 -----NCG-LYSSGWFDPDCLSANLNGKYYHQKRYGVRNGIFWGTWPGVNSLDGKC 416
QY 375 VSMKIRMYNP 385
D 417 SFQAKMMIRP 427

RESULT 9
US-08-740-223A-12
; Sequence 12; Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed ligand - vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: hTLL1
; LOCATION: 1...490
; OTHER INFORMATION: human TIE-2 ligand 1
US-08-740-223A-12

Query Match
Best Local Similarity 19.3%; Score 405.5; DB 4; Length 490;
Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

QY 23 YQNCVYHSTDSVYNIYEDGSKNAKDESKSDTYCKEDCESQVTKIRIREEHFKCRN 82
D 108 IQQNAVONHT---ATMLEIGTSLISQF-----AEQTRKLTVDYEVQVNLNGTSRLEIQL 156
```

QY 83 LONSIYSV-----TRSTFKLLRNMM 102
|:|:|:|:|
Db 157 LENSISTYLEKOLLOQTNEILIKHEKNSLLEKILMEGKHEEDLTKEEKENLOGLV 216
QY 103 DEQASLDYLSNOVN-----ELM-----NRVLLLTTEVF-----RKOLDPPP 139
|:|:|:|:|
Db 217 TRQTYIIQLEKQLNATNTNSVLOKOLELMDTVNVLNLTCKEYLLGGRKEEKP- 275
QY 140 HRPVOSHGLDCTDIDKTISVTKTPSGLYIIPBGSSTPEVWCDMDYRGCGTVYQKRI 199
|:|:|:|:|
Db 276 -----RDCADYV-----QAGFNKSGITYIYINNPEPKYFCNNDVNGGVTYIOHBE 323
QY 200 DGIIDFORLACDYLDGFGDLGEPFLGLKPIFYVNOKNTSFLVYALBSEDOTLAASY 259
|:|:|:|:|
Db 324 DGSIDPQRKWEKKEKMGFGPSEGYMLGNEFIFALTSQR--QYMLRIELMDWESNRAYSQ 381
QY 260 DNFWEDETRFEMKHLGRYSNGNDAFRGLKREDN--QNAPESTSDVNDGCRPAC--L 315
|:|:|:|:|
Db 382 DRFHIGNEKONYRLYLKHTGTAG-----KOSLILHGADSTKADANDNMCCKCALM 434
QY 316 VNGQSVKCSHLHNKTGMWFNECGLANLNGIHHS-----GKLATGIQGTWTKNNSPVK 371
|:|:|:|:|
Db 435 LRG-----GWMFDACGSPNLGMFTYAGQNNHKL--NGIKWHYF--KGPSTYS 477
QY 372 IKSVMKIR 380
|:|:|:|:|
Db 478 IRSTMMIR 486

RESULT 10

US-09-709-188-12

Sequence 12, Application US/09709188

Patent No. 6441137

GENERAL INFORMATION:

APPLICANT: Davis et al.

TITLE OF INVENTION: Expressed Ligand - Vascular Inter cellular Signaling Molecule

FILE REFERENCE: REG 333-Z

CURRENT APPLICATION NUMBER: US/09/709,188

PRIORITY FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 08/740,223

PRIORITY FILING DATE: 1996-10-25

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: 490

TYPE: PRT

ORGANISM: Homo sapiens

US-09-709-188-12

Query Match 19.3%; Score 405.5; DB 4; Length 490;
Best Local Similarity 27.5%; Pred. No. 1,4e-33;

Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQNCVHSTDSVNIIVEDGSNADESKSNDTVCKEDCEESCDVTKITREKHFMCN 82
|:|:|:|:|
Db 108 IQQNAVQNHNT-----ATMLEIGTSLSQ-----AEQTRKILDVETQVNLNOTSRLQI 156
QY 83 LONSIYSV-----TRSTFKLLRNMM 102
|:|:|:|:|
Db 157 LENSISTYLEKOLLOQTNEILIKHEKNSLLEKILMEGKHEEDLTKEEKENLOGLV 216
QY 103 DEQASLDYLSNOVN-----ELM-----NRVLLLTTEVF-----RKOLDPPP 139
|:|:|:|:|
Db 217 TRQTYIIQLEKQLNATNTNSVLOKOLELMDTVNVLNLTCKEYLLGGRKEEKP- 275
QY 140 HRPVOSHGLDCTDIDKTISVTKTPSGLYIIPBGSSTPEVWCDMDYRGCGTVYQKRI 199
|:|:|:|:|
Db 276 -----RDCADYV-----QAGFNKSGITYIYINNPEPKYFCNNDVNGGVTYIOHBE 323
QY 200 DGIIDFORLACDYLDGFGDLGEPFLGLKPIFYVNOKNTSFLVYALBSEDOTLAASY 259
|:|:|:|:|
Db 324 DGSIDPQRKWEKKEKMGFGPSEGYMLGNEFIFALTSQR--QYMLRIELMDWESNRAYSQ 381

QY 260 DNFWEDETRFEMKHLGRYSNGNDAFRGLKREDN--QNAPESTSDVNDGCRPAC--L 315
|:|:|:|:|
Db 382 DRFHIGNEKONYRLYLKHTGTAG-----KOSLILHGADSTKADANDNMCCKCALM 434
QY 316 VNGQSVKCSHLHNKTGMWFNECGLANLNGIHHS-----GKLATGIQGTWTKNNSPVK 371
|:|:|:|:|
Db 435 LRG-----GWMFDACGSPNLGMFTYAGQNNHKL--NGIKWHYF--KGPSTYS 477
QY 372 IKSVMKIR 380
|:|:|:|:|
Db 478 IRSTMMIR 486

RESULT 11

US-08-740-223A-4

Sequence 4, Application US/08740223A

Patent No. 6265564

GENERAL INFORMATION:

APPLICANT: Davis, et al.

TITLE OF INVENTION: Expressed Ligand - Vascular

NUMBER OF INVENTION: Inter cellular Signalling Molecule

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/740,223A

FILING DATE: 25-OCT-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/022/999

FILING DATE: 02-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Covert, Robert J

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 333

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7400

TELEFAX: 914-345-7721

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 497 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: Internal

FEATURE:

NAME/KEY: Human TIE-2 ligand 1

LOCATION: 1...2146

OTHER INFORMATION: from T986 clone

US-08-740-223A-4

Query Match 19.2%; Score 403.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.3e-33;

Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQNCVHSTDSVNIIVEDGSNADESKSNDTVCKEDCEESCDVTKITREKHFMCN 82
|:|:|:|:|
Db 115 IQQNAVQNHNT-----ATMLEIGTSLSQ-----AEQTRKILDVETQVNLNOTSRLQI 163
QY 83 LONSIYSV-----TRSTFKLLRNMM 102
|:|:|:|:|
Db 164 LENSISTYLEKOLLOQTNEILIKHEKNSLLEKILMEGKHEEDLTKEEKENLOGLV 223

QY 103 DEQOASLDVLSNOVN-----ELM---NRVLLTTEVF-----RKOLDPEP 139
DB 224 TQOTYIQLERKOLNATNNNSVLAQKQLELMDTVHNLVLTCKEYVLKKGKREEKPEF- 282
QY 140 HRPVOSHGLDCTDINDTISVTKTPSGLYIHPGSSYPEFVWCDMDYRGGTVYQKRI 199
DB 283 -----RDQCADVY-----QAGFNKSGITYITYINNMPERPKKVCNMDVNGGTVYQIHRE 330
QY 200 DGIIDFQRLMCDYLDGFGDLLEFVLGKRIFYIVNOKNTSFMLYVALSEDDTLAYASY 259
DB 331 DCSLDPRQRMKRYKMGFGPSEGYWLGNEFIFAITSOR--QYHLRIELMDMEGNRAYSQY 388
QY 260 DNFWEDETRFRFKMLGRYSGNAGDAFRGLKKEDN--QNAPESTSDVDNDGCRPAC--L 315
DB 389 DRFHIGNEKQRYLYLKHTGTAG-----KQSSILHGADPSTDDADNDNCMCALM 441
QY 316 VNGQSVKSCSHLNKTKGMPNECGLANGLNHHFSG-----KLATGLOMGCTWTKNNSPVK 371
DB 442 LTG-----GWFMDACGPNLNGMFTYAGQNNHKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
DB 485 LRSTTMMIR 493

RESULT 12

US-09-709-188-4
Sequence 4, Application US/09709188
Patent No. 6441137
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333-2
CURRENT APPLICATION NUMBER: US/09/709,188
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 08/740,223
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-709-188-4

Query Match 19.2%; Score 403.5; DB 4; Length 497;

Best Local Similarity 27.3%; Pred. No. 2.3e-33; Mismatches 125; Indels 121; Gaps 16;

DB 23 VQNCVHSTDSVNVIVEDGSNAKDESKSNDVCKEDCESCDVTKITREKHFMCRN 82
DB 115 IQONNAVQNH-----ATMLEIGTSLSQ-----AQTRKLDVETQVLANQTSRLEIOL 163
QY 83 LQNSIVSY-----TRSTKLLRNMM 102
DB 164 LENSISTYKLEKOLLQOTNEILKIHENKSLLEHKIILEMEGKHKEEIDTLKEEKENIQLGV 223
QY 103 DEQOASLDVLSNOVN-----ELM---NRVLLTTEVF-----RKOLDPEP 139
DB 224 TQOTYIQLERKOLNATNNNSVLAQKQLELMDTVHNLVLTCKEYVLKKGKREEKPEF- 282
QY 140 HRPVOSHGLDCTDINDTISVTKTPSGLYIHPGSSYPEFVWCDMDYRGGTVYQKRI 199
DB 283 -----RDQCADVY-----QAGFNKSGITYITYINNMPERPKKVCNMDVNGGTVYQIHRE 330
QY 200 DGIIDFQRLMCDYLDGFGDLLEFVLGKRIFYIVNOKNTSFMLYVALSEDDTLAYASY 259
DB 331 DCSLDPRQRMKRYKMGFGPSEGYWLGNEFIFAITSOR--QYHLRIELMDMEGNRAYSQY 388
QY 260 DNFWEDETRFRFKMLGRYSGNAGDAFRGLKKEDN--QNAPESTSDVDNDGCRPAC--L 315
DB 389 DRFHIGNEKQRYLYLKHTGTAG-----KQSSILHGADPSTDDADNDNCMCALM 441

QY 316 VNGQSVKSCSHLNKTKGMPNECGLANGLNHHFSG-----KLATGLOMGCTWTKNNSPVK 371
DB 442 LTG-----GWFMDACGPNLNGMFTYAGQNNHKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
DB 485 LRSTTMMIR 493

RESULT 13

US-08-373-579-4
Sequence 4, Application US/08373579
Patent No. 5650490
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-579-4

Query Match 19.1%; Score 402.5; DB 1; Length 497;

Best Local Similarity 27.3%; Pred. No. 2.9e-33; Mismatches 125; Indels 121; Gaps 16;

DB 23 VQNCVHSTDSVNVIVEDGSNAKDESKSNDVCKEDCESCDVTKITREKHFMCRN 82
DB 115 IQONNAVQNH-----ATMLEIGTSLSQ-----AQTRKLDVETQVLANQTSRLEIOL 163
QY 83 LQNSIVSY-----TRSTKLLRNMM 102
DB 164 LENSISTYKLEKOLLQOTNEILKIHENKSLLEHKIILEMEGKHKEEIDTLKEEKENIQLGV 223

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QY 103 DEQASDIYLSNVN-----ELM-----NRVLLITTEVF-----RKOLDPP 139
D 224 TRQTYIIQELKQLRATNNVLOKQOLEMDIVNLVNLCTKRVLLKGGKREEDKPF- 282
QY 140 HRPVSHGLDCTDIKDTIGSVTKTPSGLYIHPBGSSYPFEVMDMDYRGGMVYIQR 199
D 283 -----RDCADY-----QAGFNKSGIYIYINNMPPEKKVFCMMDVNGGGMVYIQR 330
QY 200 DGIIDFORLWCDYLDGFDLLGEFNLGLKIFVIYVQKNTSFMVLALESEDDTLAVASY 259
D 331 DGSIDFQGWKREYKMGFGNPGSEYWLGNFIFATISQR--QYMLIELMDMGNRAVASY 388
QY 260 DNFWEDETRFFKMHILGRYSGNAGDAFRGLKEDN--QNAPEFSISDVNDGCRPAC--L 315
D 389 DRFHGNKQNVRLYLKGTGTAG-----KQSLILHGADFSYKDDADNDNCMKCALM 441
QY 316 VNGQSVKSCSHLHNTGWMFNECGLANINGIHFS---GKLLATGIOMGTWTKNNSPVK 371
D 442 LTG-----GWMFDACGPSNLGMFYTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
D 485 LRSTTMIR 493

RESULT 14
US-08-418-595-4
: Sequence 4, Application US/08418595
: Patent No. 5814464
: GENERAL INFORMATION:
: APPLICANT: Davis, et al.
: TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/418,595
: FILING DATE: 06-APR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,579
: FILING DATE: 17-JAN-1995
: APPLICATION NUMBER: US 08/353,503
: FILING DATE: 09-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,492
: FILING DATE: 02-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,261
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/319,932
: FILING DATE: 07-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Cobert, Robert J.
: REGISTRATION NUMBER: 36,108
: REFERENCE/DOCKET NUMBER: REG 330-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 345-7400
: TELEFAX: (914) 345-7721
: INFORMATION FOR SEQ ID NO: 4:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 497 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-418-595-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.9e-33;
Matches 117; Conservative 66; Mismatches 125; Gaps 16;

QY 23 VQGNVHNHSTDSVYNIYEDGSNADESKNDYVCEKCEESCDYKRTITEKEHFMGRN 82
D 115 IQQNAVQNHNT-----ATMLEIGTSLSTQ-----AEQTKLTVETVYLVNQTSLRLETQL 163
QY 83 LQNSIVSY-----TRSTKLLRNMM 102
D 164 LENSLSYKLEKQLLQOTNEILKHEKNSLLEHKILEMGKHEBDDTLKEKENLQGLV 223
QY 103 DEQASDIYLSNVN-----ELM-----NRVLLITTEVF-----RKOLDPP 139
D 224 TRQTYIIQELKQLRATNNVLOKQOLEMDIVNLVNLCTKRVLLKGGKREEDKPF- 282
QY 140 HRPVSHGLDCTDIKDTIGSVTKTPSGLYIHPBGSSYPFEVMDMDYRGGMVYIQR 199
D 283 -----RDCADY-----QAGFNKSGIYIYINNMPPEKKVFCMMDVNGGGMVYIQR 330
QY 200 DGIIDFORLWCDYLDGFDLLGEFNLGLKIFVIYVQKNTSFMVLALESEDDTLAVASY 259
D 331 DGSIDFQGWKREYKMGFGNPGSEYWLGNFIFATISQR--QYMLIELMDMGNRAVASY 388
QY 260 DNFWEDETRFFKMHILGRYSGNAGDAFRGLKEDN--QNAPEFSISDVNDGCRPAC--L 315
D 389 DRFHGNKQNVRLYLKGTGTAG-----KQSLILHGADFSYKDDADNDNCMKCALM 441
QY 316 VNGQSVKSCSHLHNTGWMFNECGLANINGIHFS---GKLLATGIOMGTWTKNNSPVK 371
D 442 LTG-----GWMFDACGPSNLGMFYTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
D 485 LRSTTMIR 493

RESULT 15
US-08-665-926-4
: Sequence 4, Application US/08665926
: Patent No. 5851797
: GENERAL INFORMATION:
: APPLICANT: Valenzuela et al.
: TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10591-6707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,926
: FILING DATE: 19-JUN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Robert J. Cobert
: REGISTRATION NUMBER: 36,108
: REFERENCE/DOCKET NUMBER: REG 330-H

```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-2113
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 497 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-926-4

Query Match 19.18; Score 402.5; DB 2; Length 497;
 Best Local Similarity 27.38; Pred. No. 2.9e-33;
 Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQNCVHSTDSVNVNVEDSGSNKDESKSNDYCKEDCESDVKTRITREKHFMCRN 82
 Db 115 IQNNAVONHT---ATMLEICTSLISQT-----AEQTRKLTIVETQVLNQTSLREIQL 163
 QY 83 LQNSIVSY-----TRSTKLLRNMM 102
 Db 164 LENSLSYTKLEKQLQQTNEILKHEKNSLLEHKILEMEGKHKELDTLKREKENLQGLV 223
 QY 103 DEQASLDYLSNOVN-----ELM---NRVLLTTEVF-----RKQLDPP 139
 Db 224 TRQTYIIQELKEKQLNRATNNNSVLOKQOLELMDYVHNLVNLCTKEVLLKGGKREEDKPF 282
 QY 140 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIIHPGSSSYPEFVCMGDMOYRGSGWTYIOKRI 199
 Db 283 -----RDCADY---QAGFNKSGITYIYIINNMEPKVFCNMVDVGGGWTVIQHRE 330
 QY 200 DGIIDFQRLMCDYLDGFGDLGEPFLGLKIFYIVNOKNTSFMLYVALESEDDTLAVASY 259
 Db 331 DGSIDFQRGWKEYKMGFNGPGEYWLGNFIFATLSQR--QYMLRIELMDWEGNRATYSQY 388
 QY 260 DNFLEDETRFFKMHGLGKRYSGNADAFRLGKLEDN--ONAMPFSTSDVDNDGCRPAC--L 315
 Db 389 DRFHIGNEKQVRLYLGHGTGTAG-----KQSSLLHGADFSTKDADNDNCMKCALM 441
 QY 316 VNGSVKSCSHLHNKGTGWFNECGLANLNGIHHS---GKLLATGIQMGTWTKNNSPVK 371
 Db 442 LTG-----GHWFPACGSPSNLNGMFTAGQNHGKL--NGIKWHYF--KGPSYS 484
 QY 372 IKSVSMKIR 380
 Db 485 LRSTTMMIR 493

Search completed: December 16, 2002, 17:36:52
 Job time: 14.3175 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:58 ; Search time 14.6032 Seconds
(Without alignments)
2422.587 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000
Sequence: 1 EYVQGNCHVHSTDDSVYNTV.....PVKIKSVSMKIRRMNPFYK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	20.7	439	2 I37391	fibrinogen-like pr
2	405.5	20.3	432	2 A27447	cytotoxic T-lympho
3	401.5	20.1	432	2 I56934	fibrinogen-like pr
4	397	19.9	312	2 JN0596	fibrinogen-like pr
5	394.5	19.7	468	1 FGBOB	fibrinogen beta ch
6	375.5	18.8	491	1 FGHUB	fibrinogen beta ch
7	371.5	18.6	437	1 FGHUG	fibrinogen gamma-A
8	371.5	18.6	453	1 FGHUGB	fibrinogen gamma-B
9	371.5	18.6	463	2 A38463	fibrinogen beta ch
10	370	18.5	479	2 A25052	fibrinogen beta ch
11	365	18.2	444	2 S05313	fibrinogen gamma-B
12	360	18.0	432	2 FGLMG	fibrinogen gamma-B
13	352.5	17.6	438	2 A32670	fibrinogen gamma c
14	350.5	17.5	282	2 A35084	fibrinogen gamma c
15	348.5	17.4	774	2 A39832	fibrinogen-related
16	346.5	17.3	328	2 A05299	scabrous locus (sc
17	337.5	16.9	866	2 D44234	fibrinogen beta ch
18	330	16.5	1356	2 A45445	fibrinogen alpha c
19	329	16.4	334	2 JC5980	janusin precursor,
20	328.5	16.4	641	1 A41932	fibrinogen precursor
21	327.5	16.4	1353	1 JH0675	fibrinogen alpha-I
22	312	15.6	323	2 A47172	restictin precurs
23	311.5	15.6	457	1 FGRGTA	transforming growt
24	311.5	15.6	445	1 FGRGTA	fibrinogen gamma-A
25	311	15.6	4135	2 T42629	fibrinogen gamma-B
26	310.5	15.5	1810	1 A32230	tenascin-X - bovin
27	304.5	15.2	1914	2 T42635	tenascin X precurs
28	303.5	15.2	326	2 S61517	tenascin-1 precurs
29	302.5	15.1	356	1 A40701	tenascin-X precurs

30	299	14.9	417	2 S65944	tenascin-X - pig (
31	296	14.8	220	2 S28170	tenascin homolog -
32	295	14.8	326	2 B47172	ficollin-beta - pig
33	286	14.3	860	2 I48839	tenascin-X - mouse
34	284.5	14.2	2019	1 J01322	tenascin precursor
35	283.5	14.2	4008	2 T09070	probable tenascin
36	282.5	14.1	1746	1 A31694	tenascin precursor
37	271	13.6	2201	2 A32160	tenascin-C - human
38	212.5	10.6	463	2 T15876	hypothetical prote
39	180.5	9.0	915	2 T21773	hypothetical prote
40	180.5	9.0	927	2 T21772	hypothetical prote
41	173	8.6	431	2 T29850	hypothetical prote
42	154.5	7.7	933	2 A31930	cytotactin - chick
43	128.5	6.4	452	2 T26827	hypothetical prote
44	117	5.9	127	2 PC2036	microfibril-associ
45	110.5	5.5	4588	2 T28667	dyein beta heavy

ALIGNMENTS

RESULT 1

I37391
fibrinogen-like protein expressed in T lymphocytes (PT49) - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I37391; #S47273
R:Ruegg, C.; Pytel, R
Gene 160, 257-262, 1995
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A:Reference number: I37391; MUID:95369700; PMID:7642106
A:Accession: I37391
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <RES>
A:Cross-references: EMBL:Z26531; NID:9535184; PIDN:CAA85298.1; PID:9535185
A:Note: submitted to the EMBL Data Library, August 1994
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;210-435/Domain: fibrinogen beta/gamma homology <PBG>

Query Match	Best Local Similarity	Score	Pred. No.	Length
20.7%	30.2%	413.5	DB 2;	439;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;				
QY 14	SSVNIYEDGSMARDESKNDTVCKEDQ-----ESCQYKTK 50			
DB 73	SRIEVEKKEVONLKEIYNLSKKSC-QDCKIQADNGDPGRNGLLPSTGAPGEVDNKR 131			
QY 51	ITREKHEKMCNQLONS---IVSYRSTYKLLLRN-----MDEQASLDYLSNQVELM 100			
DB 132	ELESEVKNKLSELNKAKEIIVLHGRLEKLNLYMNNINENYVDSKVNLTFFVNSLDGKC 191			
QY 101	NRULLITTEYFRKQLDPEPPRPVOSHGL--DCTDIKDTIGSVTKPSGLYTIHPEGSSYP 158			
DB 192	SKC-----PSQEQIQRVVO-HLIYKDCSDYY---AIGKRSEETRYVTPDPNNSS 237			
QY 159	FEVWCDMDYRGSGWTYIOKRIDGIIDFQRLCQDVLGSGDGLGPFWIGLKIRFIYVQNK 218			
DB 238	FEVCDMETMGSGWTYIQARLDGSTNFTFTWQDKAGFGNLRREFWLGNDDTHILLT--KS 295			
QY 219	TSFMLYVALESEDDTLVASYDNFMLEDETRFEKMLGRYSNGNGDAFRGLKEDNONAM 278			
DB 296	KEMILRIDLEDFNGVEIYALDYQYVANEFLKYLRLHGVNVTAGDALR-FNKRYNNDLK 354			
QY 279	PFSTSDVNDGCRACLVNGQSVKSCSHLAKTKTGMWNECGLANWG-IHFGSKLLATG 337			
DB 355	FTTPDKNDRYPSG-----NCG-LYYSSQMWPDACLASNLNKGYYHOKRYGVANG 404			
QY 338	IOWGTW--TKNNSPVKIKSVSMKIRRMNPFYK 368			
DB 405	IFWGTWPGVSEAHPGYKSSFEKAKMIRPKHF 438			

RESULT 2

A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
A:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A>Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:8715527; PMID:3550794
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <KOY>
A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 20.3% Score 405.5; DB 2; Length 432;
Best Local Similarity 35.4%; Pred. No. 1.2e-24;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

Db 78 LRNMDEQA-----SLDLSNQVNLNNRVLLTFTEFRKQLD-----PFP 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
137 LKNKKDOIGLOGRLFTLHLYNMNNIENYVDNKVANLTVV--NSLDCKSCSKPSQHMQ 194
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 HRVOSHGL--DCDDIKDTIGSVTKTPSGLIYIHDESSYPEEVCMDRGGGVTIQK 177
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 195 SQPVQ-HLIYDKSD-HYVLG---RRSSGAYRVPRDHNSFEYVCDMETMGGWTLQA 249
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 178 RIDGIIDQRIMCDYDLDFGDLGFWMGLKRIPIYNOKNTSPFLYALSEDDTLAYA 237
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 RLDSSTNTRRMKDVKAFGEFMLEREFWLGNDKIHLTT--KSEMILRIDLFDFNGLTLYA 307
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 238 SYDNWEDEETREFEMHGIRYSGNAGDAFRGLKEEDNONAPFSTDVNDGCRACLVN 297
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 308 LYDQRYANEFLLKRLHIGNYNGTAGDLR-FSRRIYNHDLFFPTTPPDNDNRYPBG---- 362
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 238 GOSVKSCHLHNKTGMWFNECGLANLNG-IHFSGKLATGISOMGTWTNRN--SPVKIKS 354
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 363 -----NCG-LYYSSGMPDSCLSANLNCKYHKYKGVANGIFMCTMGINGINAOAGGYKS 416
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 355 VSMKRIRMKNP 365
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 417 SFKKAKMIIP 427
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 3

I56934
fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
A:Accession: I56934
R:Peir, R.L.; Fung, L.; Reneker, J.; Myers-Watson, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A>Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induced
A:Reference number: I56934; MUID:95333285; PMID:7609073
A:Accession: I56934
A>Status: preliminary; translated from GB/EMBL/DDB
A:Molecule type: mRNA
A:Residues: 1-432 <RBS>
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics:
A:Gene: musfibp
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 20.1% Score 401.5; DB 2; Length 432;
Best Local Similarity 35.0%; Pred. No. 2.6e-24;
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

Db 78 LRNMDEQA-----SLDLSNQVNLNNRVLLTFTEFRKQLD-----PFP 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
137 LKNKKDOIGLOGRLFTLHLYNMNNIENYVDNKVANLTVV--NSLDCKSCSKPSQHMQ 194
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

[illegible]

A:Molecule type: mRNA
A:Residues: 276-437 <KAN>
R:Forname Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379; PMID:6092346
A:Accession: B92448
A:Molecule type: DNA
A:Residues: 286-437 <FOR>
R:Mam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A:Title: Isolation and characterization of cDNA clones for the Alpha- and gamma-chains
A:Reference number: I37393; MUID:84069777; PMID:6689067
A:Accession: I37393
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 209-270 <RES>
R:Bertagnoli, M.E.; Beckele, W.C.
J. Cell Biol. 121, 1329-1342, 1993
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
A:Reference number: A40698; MUID:93286185; PMID:8509453
A:Accession: A40698
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <BER>
A:Experimental source: thrombin-activated platelets
A:Note: sequence extracted from NCBI backbone (NCBIP:133734)
R:Kuntzake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigore, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A:Reference number: A54223; MUID:94162201; PMID:8117655
A:Accession: H54223
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <KUN>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370; PMID:6575689
A:Contents: annotation; review; disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; C
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
R:Blomback, B.; Hessel, B.; Hoger, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080; PMID:936108
A:Contents: annotation; disulfide bonds
R:Hoeprich, P.D.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1983
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds
A:Reference number: A90467; MUID:83221465; PMID:6860649
A:Contents: annotation; quaternary structure, disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Horwitz, B.H.; Varadi, A.; Scheraga, H.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A:Reference number: A94006; MUID:85014892; PMID:6592597
A:Contents: annotation; polymerization region
R:Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-1774, 1984
A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure
A:Reference number: A90483; MUID:84203545; PMID:6326808
A:Contents: annotation; platelet aggregation region
R:Plow, E.F.; Strouff, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.
J. Biol. Chem. 259, 5388-5391, 1984
A:Title: Evidence that three adhesive proteins interact with a common recognition site o

A:Reference number: A92477; MUID:84185664; PMID:6325435
A:Contents: annotation; platelet aggregation region
R:Dang, C.V.; Ebert, R.F.; Bell, W.R.
J. Biol. Chem. 260, 9713-9719, 1985
A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit post
A:Reference number: A92549; MUID:85261382; PMID:3160702
A:Accession: A92549
A:Contents: annotation; calcium binding region
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH
A:Reference number: A37117; MUID:80337977; PMID:2143188
A:Contents: annotation; hemectin cleavage site
A:Note: hemectin, a protease from Haemophilus phagocytans, the giant South American l
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: The two forms of gamma chain, A and B (see PIR:FGHGB), arise by alternate
intron, which makes this chain different from the gamma-B chain at positions 434-437
A:Gene: GDB:FCG
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
E:1-26/Domain: signal sequence #status predicted <SIG>
E:27-437/Product: fibrinogen gamma A chain #status experimental <MP>
E:116-415/Domain: fibrinogen beta/gamma homology
E:341-355/Domain: calcium binding #status predicted <CAB>
E:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
E:423-437/Region: platelet aggregation site, status predicted
E:34/Disulfide bonds: interchain (to gamma-35) #status experimental
E:35/Disulfide bonds: interchain (to gamma-34) #status experimental
E:45/Disulfide bonds: interchain (to beta-110) #status experimental
E:45/Disulfide bonds: interchain (to alpha-64) #status experimental
E:78/Binding site: carbohydrate (asn) (covalent) #status experimental
E:161/Disulfide bonds: interchain (to beta-227) #status experimental
E:165/Disulfide bonds: interchain (to alpha-180) #status experimental
E:179-208,352-365/Disulfide bonds: #status experimental
E:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimen
E:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental
Query Match 18.68; Score 371.5; DB 1; Length 437;
Best Local Similarity 31.98; Pred. No. 6.6e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
QY 65 NSIVSYRSTKLLRNMDQ-----QASLDYLSNOYNEILNVLTLTVEFRKQIDPF 118
DB 103 NMIDAATLKSRLMEIIMKYEASTILTHDSSIRYLQEIYNSNQNIVNKEV--AQLEAQ 160
QY 119 PHRP-----VQSH---GLDCTDIKDTIGSVYKTPSGLYTIHPEGSSYPPEVWCMQDNRGG 171
DB 161 CQEPCKDTIVQIHDITGKDCQD-----INKGAKQSGGLFYIKLKNQOFLVYCEIDGSGNG 216
QY 172 WTVQKRIKIDGIIDRQRLMCDVLDGFGD-----LGEFNLGKIKFYINQKTSMLVYAL 227
DB 217 WTVQKRIKIDGIVDKKNIWIKYKRGFGLSPGTTIEFNLGKIKHILISTQSAIPALRYEL 276
QY 228 ESEDDTIAYASYNDFWLEDETRFKMLIGRYS--GNAGDAFGLKRED-----NONAM 278
DB 277 EDWNGRISTADYAMFKVGPEDAKYRLVAYAPAGDAGAFDGFDPGDDPSDKPFTSHNGM 336
QY 279 PFSTSDVDNDCGRACLVNGQSVASCSHLNKTGWMEFEGCLANGLIHHSGLV----- 333
DB 337 QFSTWMDNDKFEKNGCAEDQGS-----GWMNKKCHAGHLNGVYOGGTYSKAST 385

OY 334 ---LATGIOMGTWTNNSPVKIKSVSMKI 359
Db 386 PNGYDNGIIMATW--KTRWYSMKKTMTKI 412

RESULT 8

FGHUGB
Fibrinogen gamma-B chain precursor [validated] - human
NAlternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
C:Accession: A90494; A90448; A90453; A28203; B28203; I37390; A03126
R:Rikun, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774; PMID:2990550
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1113,'T',115-453 <R1X>
A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PIDN:AAB595
R:Rosenberg, J.R.; Cummins, D.E.; Comeau, C.M.; Kanf, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379; PMID:6092346
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <ROR>
R:Mollenstein-Yodel, C.; Moseson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068933; PMID:7306501
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <WOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: A94194; MUID:86217900; PMID:3368448
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453 <FR2>
R:Marchetti, L.; Zanello, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334; PMID:1685103
A:Accession: I37390
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:931410; PIDN:CAA3837.1; PID:9931064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate splicing, which makes this chain different from the gamma-B chain at positions 434-437 and C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plasmas.
A:Gene: GDB:FCG
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-q428
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGHUG) and beta chains. Two three-chain coiled coils emerge from this core and coiled from the distal domain.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein; F:1-76/Domain: signal sequence #status predicted <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPY>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>

F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of F:34/Disulfide bonds: Interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: Interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: Interchain (to beta-110) #status predicted
F:49/Disulfide bonds: Interchain (to alpha-64) #status predicted
F:78/Binding site: carboxylate (Asn) (covalent) #status predicted
F:161/Disulfide bonds: Interchain (to beta-227) #status predicted
F:165/Disulfide bonds: Interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: Isopeptide (Gln) (Interchain to Lys-432 N6-amino) #status predicted
F:432/Cross-link: Isopeptide (Lys) (Interchain to Gln-424) #status predicted

Query Match 18.6% Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 6.9e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

OY 65 NSIVSTRSTKKLLRMMDQ-----QASLYLSNOVVELMNRVLLTTEVFRQQLDF 118
Db 103 NMIDAATLTKSRKMLEERIMKYEASILTHDSIRYLOEIVYNNQKIVNLEKY--AQLENO 160
OY 119 PHRP---VQSH---GLDCTDIKDTIGSVTKPSGLYIHPGSSVPFVCMQMDYRGSG 171
Db 161 CGEPCKDTYQHHDYICKDQD---IANKGAKOSGLYFKPLKANOQFLVCEIDGSGNG 216
OY 172 WTVIQKRIIDGIDFORLWCDYLDGFGDL---LGEFGLGKRIFYIVNOKNTSMILYVAL 227
Db 217 WTVEFGKRLDGSVDYFKKNWIOYKEGFGHLSPTGTTERWLGNEKHILHISQALPYALRVEL 276
OY 228 ESEDDTLNAAVDNFWLDEETREFKHLGRYS-GNAGDAFRLKEDK-----NONAM 278
Db 277 EWMNGRTSTADYAMFVGEADKRYLTYYAFAGGADGDFDFGDDPSDKFTFSHNGM 336
OY 279 PESTSDVDNDGCRPACTLVAGSGVSCSHLNKTKGMWNECGLANLNGIHFFSGKL----- 333
Db 337 QSTWMDNDKDRKGNCAEDDGS-----GWMNKHCHGHLNGVYGGSTYSKAST 385

OY 334 ---LATGIOMGTWTNNSPVKIKSVSMKI 359
Db 386 PNGYDNGIIMATW--KTRWYSMKKTMTKI 412

RESULT 9

A38463
Fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
R:Welsbach, L.; Oddoux, C.; Procyk, R.; Grleninger, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745; PMID:2009266
A:Accession: A38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEL>
A:Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.6% Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 7.1e-22;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;

OY 41 CEESCDVTKTIREKHF--KCRNLONSIVSY--TRSTKKLLRMMD----- 83
Db 80 CPTGCELTTLTKOKETVYPVLDRKVRKESDSTWYQYVNMIDMKLVYTKQRKDN 139
OY 84 -----EQGASLDYLSNOVVELMNRVLLTTEVFRQQLDFPHRPVQS----- 125
Db 140 DIILSEYNTMELHNYIKNDNNIPSSLRVLRVAVDSL-HKKTKOLENAIATOTDYCR 198

Oy 126 -----HGLDCTDKDTIGSTKTPPSGLYIIHPGSSYPFEVMCDMDYRGSGT 173
 Db 199 SPVCASCNIPVSGRECEDEYIRKGET-----SEMYIIOPDEFTPYRYKCMETDNGMT 254
 Oy 174 VIOKRIDGIIDFORLMCDYLDGFG-----DLGFEWLGKIKFYIVNOKNTSFM 222
 Db 255 LIQNRQGSVNFEGAMDEYKRGFNIAKSGKKYCDIPGEVWLGNDKISQITKGPFR-- 312
 Oy 223 LVALESED---DTLAAVSDNFWLEDETRFEKMLHGRYSGNADAF---RGLKEDN- 274
 Db 313 --VLIEEMDNWNGDKVS-ALYCGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRT 369
 Oy 275 ---QNAPEFSTDVDNDCGRPACLYNGOSVSCSHLNKTKWMEGGLANLNGIHHSFG 331
 Db 370 MTIHNGMYFSTYDRDNG-----WLTDPDRKQCSK-EDGGGGMWYNRCHAAPNNGRYWGG 423
 Oy 332 KL-----LATGIQGTWTKNNSPVKIKSVSKIRMYNPF 367
 Db 424 TYSMDAKHGTDCIYVMNM--KGSWYSKMKMSMKIK----PYF 461

RESULT 10

A25052
 fibrinogen beta chain - sea lamprey (fragments)
 N:Contains: fibrinopeptide B
 C:Species: Petromyzon marinus (sea lamprey)
 C>Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
 C/Accession: A25052; A03124; B03124
 R:Bohous, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
 Biochemistry 25, 6512-6516, 1986
 A>Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
 A:Reference number: A25052; MUID:87076582; PMID:3790537
 A:Accession: A25052
 A:Molecule type: mRNA
 A:Residues: 39-479 <BOH>
 A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
 R:Cottrell, B.A.; Doolittle, R.F.
 Blood. Biophys. Acta 453, 426-438, 1976
 A>Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
 A:Reference number: A03120; MUID:77065679; PMID:999898
 A:Accession: A03124
 A:Molecule type: protein
 A:Residues: 1-36 <COT1>
 A:Accession: B03124
 A:Molecule type: protein
 A:Residues: 37-42 <COT2>
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C:Keywords: blood coagulation; glycoprotein; sulfoxide
 F:1-36/Product: fibrinopeptide B #status experimental <FBP>
 F:37-479/Product: fibrin beta chain #status experimental <MAT>
 F:50-219/Domain: fibrinogen disulfide ring homology <FBG>
 F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
 F:13/Binding site: sulfate (TYR) (covalent) #status experimental
 F:27/Binding site: carbohydrate (ASN) (covalent) #status experimental

Query Match

Best Local Similarity 18.5%; Score 370; DB 2; Length 479;

Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;

Oy 25 NAKESKSNITVCKEDE-----ESCDYKTKITREKHFMRNLONSIVSTYRS 73
 Db 130 NSFDPMASDSTLKNQVOTLRRRLNSSSTHVNAKOKELENRYKVKIR-TESTVAGSLRS 188
 Oy 74 TKLLRMNMEQOASLDYLSNQVNLNMRVLLTTEVFRKQLDPEFPHRVSGLDCTDI 133
 Db 189 MKSVLEHLRAKMQMEKAIKTQ-KELCSAPCTVACRY-----PVVS-GMHCEDI 235
 Oy 134 KDTIGSTKTPPSGLYIIHPGSSYPFEVMCDMDYRGSGWTVIQKRIDGIIDFORLMCDYL 193
 Db 236 YRNGGRSTSEA---YTIQPDLFSEPRYKVCDFMESHGSGWTVQNRVDSGSNFARDMWTYK 291
 Oy 194 DGFGLD-----GEFWLGKIKFYIVNOKNTSFMILVLESDDTLAAVSDNF 242

Db 292 AEFNIAFGNKSICNIPGEWLGTKYHQLTKO-HTQOVLFDMSDWEGSSV-YAQTASF 349
 Oy 243 WLEDETRFEKMLHGRYSGNADAF-FRGLK--EDNO-----NAMPFSTDVDNDCGRPAC 294
 Db 350 RPEMDAQGYRLWVEDYSGNAGNALLLEGATOLMGDRWRTIHNGQFSTFDDNDNMNM-- 407
 Oy 295 LVNGOSVSCSHLNKTKWMEGGLANLNGIHHSFG---KLA-----TGIQGTWTKN 346
 Db 408 ---GDPTRKCSR-EDAGGGMWYNRCHAAPNNGRYWGGIYTRKQADYCTDDGVVMNM--K 461
 Oy 347 NSPVKIKSVSKIR 360
 Db 462 GSWYSKMKMSMKIK 475

RESULT 11

S05313
 fibrinogen gamma-B chain precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
 C/Accession: S05313
 R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
 Nucleic Acids Res 17, 6397, 1989
 A>Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinogen
 A:Reference number: S05313; MUID:8936676; PMID:2711651
 A:Accession: S05313
 A:Molecule type: mRNA
 A:Residues: 1-444 <BRO>
 A:Cross-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350
 A>Note: The authors translated the codon AGT for residue 105 as Ala and ART for resid
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
 F:174-414/Domain: fibrinogen beta/gamma homology <FBG>

Query Match

Best Local Similarity 18.2%; Score 365; DB 2; Length 444;

Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;

Oy 65 NSIYSTRSTKRLRNMM-----DEQASLDYLSNQVNLNMRVLLTTEVFRKQLDPE 118
 Db 101 NIESATNKSMSMEIKYETLISTHESTRFQDEYVNSQKIVNLRDLYV--QLEAN 158
 Oy 119 PHRPVQ-----HGLDCTDKDTIGSTKTPPSGLYIIHPGSSYPFEVMCDMDYRGSG 171
 Db 159 QCEPQODTVKIDHTYGRQCD---VANAKAKESGLYTRPL-KAKGYLVCEIDSGSG 213
 Oy 172 WTVIQKRIDGIIDFORLMCDYLDGFGDL-----GEFWLGKIKFYIVNOKNTSFMILY 225
 Db 214 WTVQKRIDGSLDPKKNIOYKEGFGHLSPTGTGTEFWLNEKIHILISTOSIPLYLRI 273
 Oy 226 ALSEDDTLAAVSDNFWLEDETRFEKMLHGRY-SGNAGDAFRLKAKED-----NON 276
 Db 274 QLEDMNGRTSTADYASEFVGTGENDYRLTYVYFGGDGDFDGDGDDSDSKFFTSYHN 333
 Oy 277 AMPFSTDVDNDCGRPACLYNGOSVSCSHLNKTKWMEGGLANLNGIHHSGLLAT 336
 Db 334 GMDSTHMSQNDKDKDNC---AEQY-----GIGMMNMCHAGHLNGVYVGCGTYSKT 382
 Oy 337 -----GIQGTWTKNNSPVKIKSVSKIR 359
 Db 383 STPNGYDNGIIMATW--KSRWYSKMKIKTYMKI 411

RESULT 12

FGLMGS
 fibrinogen gamma chain precursor - sea lamprey
 C:Species: Petromyzon marinus (sea lamprey)
 C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 20-Oct-2000
 C/Accession: A03129
 R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohous, V.L.; Pontes, M.; Evans, B.; Rile
 Biochemistry 24, 92-101, 1985
 A>Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general charac

A:Reference number: A03129; MUID:85199776; PMID:2581603
A:Accession: A03129
A:Molecule type: mRNA
A:Residues: 1-432 <STR>
A:Cross-references: GB:K03049; NID:9213193; PIDN:AAA49262.1; PID:9213194
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-432/Product: fibrinogen gamma chain #status experimental <MP>
F:175-411/Domain: fibrinogen beta/gamma homology <FBG>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:227/Binding site: carboxylate (Asn) (covalent) #status predicted
F:421/Cross-link: isopeptide (Gln) (interchain to Lys-425 N6-amino) #status predicted
F:425/Cross-link: isopeptide (Lys) (interchain to Gln-421) #status predicted

Query Match 18.0%; Score 360; DB 1; Length 432;
Best Local Similarity 30.1%; Pred. No. 5, 3e-21;
Matches 115; Conservative 52; Mismatches 151; Indels 64; Gaps 16;

QY 13 DSSVNIYEDGSNAKDE-SKSNDYCKEDCESCVKTKITREKIFMCRNLQNSIVSYT 71
DB 62 DSSFDISVLTQIAAKHGIVEGVNIVNED-----VITTRDAQIINDSGQKTYQKITL 113
QY 72 RSTKLLRNMDQOASLDYLS-----NQ--VNELMNRVLLLTTEYFRKQOLDPEPRPYQ 124
DB 114 EEV-RLEQIGVSHDAQIELSEMRVNOQFYTRLOQQLVDIRQTSRSCQDTANKISP 172
QY 125 SHGLDCTDIKPTIGSYTKTPSGLYIHPGSSYFEVWCMDMDYRGSGWTIVIQKRIDGIID 184
DB 173 IKGKDCQGVVDNGK-----DSGLYIKPLKAKQPELVCEIE-NGNGMTVIVQHRHDSYV 227
QY 185 FORIMCDYLDGFG-----DLGEFWLGLKIFIVYNOKNTSFMILYALSEDDTLAASVD 240
DB 228 FTRDMVSTREGFGYAPLTTLTEFWLGNKIHILTGQO--AYRLRIDLTWENHRRADYG 285
QY 241 NFWL--EDETFR-FKMHGGRYSNAGDAFRGLKEDNON-----AMPESTDVDND 288
DB 286 HKRLPESDEYRLFSMYL---DGDAGNAFDFGDFDQDKFYTHLMISTPERDND 342
QY 289 GCRPACLVNGQSVKSCSHLNKTKGMWFNCGLANLNGIHHSFGKLLAT-----GIQM 340
DB 343 KYEGSCAEODGS-----GWMNMRCHAGHLNGKYFGGNRYKRTDVEFPYDGIIM 391
QY 341 GTWTKNNSPVKIKSVSMKIRRM 362
DB 392 ATW--HDMWYSLKMTTKLLPM 411

RESULT 13
A32670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
C:Accession: A32670; I51416
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; MUID:9024182; PMID:2334684
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02894; NID:9214139; PIDN:AAA49709.1; PID:9214140
R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
A:Reference number: I51416; MUID:91146806; PMID:2289632
A:Accession: I51416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-58 <BHA>
A:Cross-references: GB:M3548; NID:9214141; PIDN:AAA03247.1; PID:9214142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.6%; Score 352.5; DB 2; Length 438;
Best Local Similarity 27.2%; Pred. No. 2, 2e-20;
Matches 106; Conservative 54; Mismatches 141; Indels 89; Gaps 14;

QY 39 EDCEESCVKTKITREKIF-----MCRNLQNSIVSYTSTKLLRNMD-----EQQ 86
DB 41 EYCPPTGISDFLNRQENVDDQLQLEMLNQINSSTGTTIIVHLIDSGKRPATSPQ 100
QY 87 ASLD-----YLSQVNELMNRVLLLTTEYFRKQOLD-PE 118
DB 101 TADPMTQSKTCMKLTDMKNYYQYEENILYQEVYSSNQNKIFLKKRIANLELQCOO 160
QY 119 PRRPV-----QSHGLDCTDIKPTIGSYTKTPSGLYIHPGSSYFEVWCMDMDYRGSGWT 174
DB 161 PCBDYVQIDFETKDCQGEVANKGARL-----SGLYIKPLKAKQPELVCEIESGSAMTV 216
QY 175 IQKRIDGIIDFORIMCDYLDGFGDL-----LGEFWLGLKIFIVYNOKNTSFMILYALSE 230
DB 217 IORLDGSVNFHKNWVQYREGFYLSPNDKTEFWLGNKIHILSTQSTIIPYVRIELDM 276
QY 231 DDTLAYASVDNFWL--EDETFR-FKMHGGRYSNAGDAFRGLKED-----NQNM 278
DB 277 SNKSTADYSTFLGSEKDNRYFTYVFTG---GDAGDAFDGDFDSDSKFTYSHNGM 333
QY 279 PESTDVDNDGCRPACLVNGQSVKSCSHLNKTKGMWFNCGLANLNGIHHSFGKL----- 333
DB 334 QFSTFDKNDKFDGCAEDGS-----GWMNMRCHAGHLNGKYFGGTYSEADS 382
QY 334 ----LATGIQMGWTNNSPVKIKSVSMKI 359
DB 383 GPSGYDNGITIMATWRRR--WYSKSVTKMI 410

RESULT 14
A35084
fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvlenensis)
C:Species: Parastichopus parvlenensis
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C:Accession: A35084
R:Xu, X.; Doolittle, R.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A:Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
A:Reference number: A35084; MUID:90192754; PMID:2315305
A:Accession: A35084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-282 <XUX>
A:Cross-references: GB:M31326; NID:9161164; PID:9161165
C:Superfamily: fibrinogen beta/gamma homology
F:67-280/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.5%; Score 350.5; DB 2; Length 282;
Best Local Similarity 36.8%; Pred. No. 1, 8e-20;
Matches 92; Conservative 31; Mismatches 96; Indels 31; Gaps 10;

QY 113 KOLDPEPRHPRVQSHGLDCTDIKPTIGSYTKTPSGLYIHPGSSYFEVWCMDMDYRGSGM 172
DB 58 KRISHPEYR-----HDCYDIIQSC-SGGSPPSGQYIIPDDGNL-IRKYCMEIDEGM 110
QY 173 TVIQKRIDGIIDFORIMCDYLDGFGDLGEFWLGLKIFIVYNOKNTSFMILYALSEDD 232
DB 111 TVFORIRDGTINFRYSMYQTFGFLNTEFWLGNINHYLNSQD--YELRVELNNTLG 168
QY 233 TLAYASVDNFWLEDERFRFKMLHGRYSNAGDAFRGLKEDNONAMPSTSDVDNDGCRP 292
DB 169 NHYAKYVNFRIQDSEFEVLVLAAGSFGAOSLA-----YHNMRFSTYDNDND---- 218
QY 293 ACLVNGQSVKSCSH-LAHNTYGMWFNCGLANLNGIH--FSGLKLTAGIQMGWTNKNSPV 350
DB 219 -----YSTINCASHSSYGGAMWYKSCLLSNLNGQYTYDYG--APSTYWSYLPDGDND-- 268

QY	351	KIKSVSMKIR	360
	:	:	
Db	269	QIPFAEMKLR	278

RESULT 15

scabrous locus (sca) protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C:Accession: A39832; S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A:Title: Spacing differentiation in the developing *Drosophila* eye: a fibrinogen-related
A:Reference number: A39832; MUID:91075223; PMID:2175046
A:Accession: A39832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-774 <BAK>
A:Cross-references: GB:M60065; GB:M37703; NID:g158401; PID:g158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A:Title: Molecular analysis of scabrous mutant alleles from *Drosophila melanogaster* ind
A:Reference number: S58998; MUID:96109607; PMID:864397
A:Accession: S58998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'T', 20-774 <HUX>
C:Genetics:
A:Gene: FlyBase:sca
A:Cross-references: FlyBase:FBgn0003326
C:Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>

Search completed: December 16, 2002, 17:36:22
Job time : 16.6032 secs

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:23 ; Search time 8.7619 Seconds

(without alignments)
1742.006 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000

Sequence: 1 EYVQGNVCHSTDSVNVIV.....PVKISVSMKIRMTNPKK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	20.7	439	1	FGI2_HUMAN
2	405.5	20.3	432	1	FGI2_MOUSE
3	400.5	20.0	481	1	AGP1_BOVIN
4	400.5	20.0	493	1	AGP2_MOUSE
5	400	20.0	493	1	AGP2_HUMAN
6	398	19.9	312	1	FGI1_HUMAN
7	395.5	19.8	468	1	FGI1_BOVIN
8	395	19.8	498	1	AGP1_HUMAN
9	391	19.6	498	1	AGP1_MOUSE
10	381.5	19.1	496	1	AGP2_HUMAN
11	375.5	18.8	491	1	FGI1_HUMAN
12	375	18.8	375	1	FGI2_BOVIN
13	374.5	18.7	496	1	AGP2_MOUSE
14	373.5	18.7	479	1	FGI1_RAT
15	371.5	18.6	453	1	FGI1_HUMAN
16	371.5	18.6	463	1	FGI1_BOVIN
17	370	18.5	477	1	FGI1_PETMA
18	365	18.2	444	1	FGI1_BOVIN
19	360	18.0	432	1	FGI1_PETMA
20	360	18.0	509	1	AGP1_MOUSE
21	358	17.9	503	1	AGP1_HUMAN
22	352.5	17.6	438	1	FGI1_XENLA
23	351	17.5	319	1	FGI1_RAT
24	350.5	17.5	782	1	FGI1_PARPA
25	348.5	17.4	774	1	SCA_DROME
26	337.5	16.9	866	1	FGI1_HUMAN
27	335.5	16.8	741	1	FGI1_CHICK
28	332	16.6	306	1	FGI1_MOUSE
29	329.5	16.5	641	1	FGI1_PETMA
30	329	16.4	334	1	FGI1_MOUSE
31	327.5	16.4	445	1	FGI1_RAT
32	321.5	16.1	313	1	FGI1_HUMAN
33	321	16.1	255	1	FGI1_HUMAN

34	313.5	15.7	782	1	FGI1_RAT	P06399
35	310.5	15.5	1808	1	TENX_CHICK	rattus norv
36	308.5	15.4	326	1	FGI1_HUMAN	P10039
37	305.5	15.3	335	1	FGI1_RAT	gallus gall
38	302.5	15.1	4289	1	TENX_HUMAN	P00602
39	291	14.5	299	1	FGI1_HUMAN	homo sapien
40	282.5	14.1	1746	1	TENX_PIG	P07566
41	271	13.6	2201	1	TENX_HUMAN	homo sapien
42	197	9.8	137	1	AGP2_RAT	P24821
43	109	5.5	129	1	FGI1_BOVIN	homo sapien
44	98	4.9	782	1	SCA_DROME	P05918
45	97.5	4.9	1432	1	SKI3_YEAST	rattus norv

ALIGNMENTS

```

RESULT 1
ID FGI2_HUMAN STANDARD; PRT; 439 AA.
AC 014314;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DE Fibrinogen-like protein 2 (PT49).
GN FGI2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytela R.; transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.*;
RL Gene 160:257-262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuvaraj S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of Hg12: the human counterpart to the
RT mouse gene Fg12.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT G1U-53.
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel G.L., Ozuna M., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=98309432; PubMed=9647217;
RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Argaves S., von Fliedner V., Pytela R., Ruegg C.;
RT "Characterization of human fibrinogen-like protein
RT secreted by T lymphocytes.";
RL J. Immunol. 161:138-147(1998).
CC -!- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC MUCOSAL SITES.
CC -!- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).

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QY 238 SYDNFWLEDETRFFKMHGKRYSGNAGDAFRGLCKEDNONAMPSTSDVNDGCRPACLVN 297
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 308 LYDPOFYVANEFLKRYLRHIGNNGTAGDALR-FSRHYNDLFFETTPDRDNRPSG---- 362
QY 298 GQSVKSGSHLNKRWMPNECCGLANLNG-IHFGSKLLATGICGTWTKNN--SPVKIKS 354
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 363 -----NCG-LYSSGWMFSDCLSNLNKGYHOKYGVKRGNGIFWGTGNGIQAOPGGYKS 416
QY 355 VSMKIRRYNYP 365
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 417 SFRQAKMIRP 427

RESULT 3
AGPL_BOVIN STANDARD; PRT: 481 AA.
AC 018920:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Angiopoietin-1 precursor (ANG-1) (Fragment).
GN ANGPT1 or ANG1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=99034348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN 12
RP SEQUENCE OF 91-200 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98451564; PubMed=976732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF093573; AAC61872.1; -.
DR EMBL: AF032923; AAC78245.1; -.
DR HSSP: P02671; 1PZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
KM Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 15 POTENTIAL.

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FT CHAIN 16 >481 ANGIOPOIETIN-1.
FT DOMAIN 153 261 COILED COIL (POTENTIAL).
FT DOMAIN 283 >481 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 481
SQ SEQUENCE 481 AA; 55556 MM; 88EC9ED84FC2B50 CRC64;

Query Match 20.0%; Score 400.5; DB 1; Length 481;
Best Local Similarity 27.9%; Pred. No. 1,4e-24;
Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;

QY 3 VQGNVHSTDTSSVYNIYEDGSNAKDESKSDNYCKECCSCDYKTKITREKHKMKN 62
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 115 IQNNAVQNH-----ATMLEIGTSLSSQ-----AEQTRKLDVEYVLNQTSLRLEIQ 163
QY 63 LQNSIVSY-----TRSTKLLRNMM 82
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 164 LENSLSYTKRKQLQOTNEILKIHENKSLLEHKIFEMEGKHKEBLDTLKEKENLQGLY 223
QY 83 DEQASLDYLSQVN-----ELM-----NRYLLITVEYF-----RKQDPFP 119
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 224 TRQYTIIDELCKQLNRATTNNSVLOKQOLEMDYVHNLVNLCTKRVLLKGGKRREKPF- 282
QY 120 HRPVQSHGLDCTDIKDTIGSVTKRPSGLYTIHPBESSYPFEVCMCDYRGGMVYQKRI 179
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 283 -----RDCADYV-----QAGFNKSGITYTYIYINMPKPKVFCMDLNGSGWVYIQHRE 330
QY 180 DGIIDFORLMDYLDGFDGLGEFWLGLKTIIFYVQNTSPMLYVALESEDDTLAVASY 239
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 331 DGSIDFQGWKEYKKGFENPSEGYLGNELFATISQR--QYTLRIELDMENRATYQY 388
QY 240 DNFWEDETRFFKMHGKRYSGNAGDAFRGLCKEDN--ONAMPSTSDVNDGCRPAC--L 295
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 389 DRFHNGEKONYRLYLKCHGTAG-----KOSLLILHGADFSTKDDNDNMCCKALM 441
QY 296 VNGSVKSCSHLNKRWMPNECCGLANLNGIHHS-----GKLLATGICW 340
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 442 LFG-----GWMFDCGPSNLNGMFTYTAGQNHKLU--NGIKW 475

RESULT 4
ANL2_MOUSE STANDARD; PRT: 493 AA.
ID ANL2_MOUSE
AC Q9R045;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin-related protein 2 precursor (angiopoietin-1-like 2).
GN ANGPTL2 OR ARP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiopoietin-
RT related protein. angiopoietin-related protein induces endothelial cell
RT sprouting.";
RL J. Biol. Chem. 274:26523-26528(1999).
CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
CC SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS
CC AND TESTIS.

```

CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC
CC EMBL: AF125176; AAD5358.1; -.
CC DR HSSP: P02671; 1FZD.
CC DR MGI:1347002; Angptl2.
CC DR InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C; 1.
CC SMART: SM00186; FBG; 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW signal; Coiled coil; Glycoprotein.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 493 ANGIOPOIETIN-RELATED PROTEIN 2.
CC FT DOMAIN 77 115 COILED COIL (POTENTIAL).
CC FT DOMAIN 152 202 COILED COIL (POTENTIAL).
CC FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 493 AA; 57118 MW; 22885ABEF0746BF2 CRC64;

Query Match 20.0%; Score 400.5; DB 1; Length 493;
Best Local Similarity 26.7%; Pred. No. 1.4e-24;
Matches 107; Conservative 66; Mismatches 107; Indels 121; Gaps 15;

OY 48 KTKITREKHEKMCRLNONSIVSTRSTKTLRMMDQASLYLSNOVELNRRVLLLT 107
DB 119 EYKULRKES-----RNNNSKV---TOLYQULHEIIRKRDNAL-----ELSQLERNILNOT 166
OY 108 TEVER-----KOLD-----PEPHRP----- 122
DB 167 ADMLQASKYKDEHKEQHLMLAHNOSEVIAQLEEHQCRVPARARMPQPRAPPRVYQ 226
OY 123 -----VQSH-----GLDCTDIKDTIGSVTKTPSG----- 146
DB 227 PPTYNRIINOISTNEIOSQONIKVLPPLPTMPALTSLSSTDKPSGPMWDCLOALEDHG 286
OY 147 -----LYIHREGSSYFEWCDMDYRGGWTVYQKRIIDGIDFORLMCDVLDGFGDLGE 202
DB 287 STSSITLVREPENTNRLMQWCDOHRDPGCVTYIQKRLDSVNFRRMWEYTKQSGFNIDGE 346
OY 203 FVLGLKRIEYVNOKNTSEMLYVALESEDDTLAYASYDNFMLEDETRFFKMLGRYSGNA 262
DB 347 YMLGLENIYVLMQGN--YKLLVTMEDWSGRKVFAYASFLREPESEYKRLRGYHGN 404
OY 263 GAFFRLKKEDNONAMPSTSDVDNDCRPACLVNCGSAKSCSHLNKKGWPNEGGLAN 322
DB 405 GGSFTW-----HNGKQFTTLDRDHD-----VYTG-----NCAH-YQKGMWYNACASHN 447
OY 323 LINGIHFSKLLA---TGIONGTWTKNNSPVKIKSYSMKIR 360
DB 448 LNCVWYRGGHYRSRYODGYVAEF--RGGSYSLLKVVMMIR 486
RESULT 5
ANL2_HUMAN
ID ANL2_HUMAN STANDARD; PRT; 493 AA.
AC O9UK09;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR AR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RA MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiopoietin-
RT related protein. angiopoietin-related protein induces endothelial cell
RT sprouting.";
RL J. Biol. Chem. 274:26523-26528(1999).
CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE,
CC SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY,
CC ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF125175; AAD5357.1; -.
CC DR HSSP: P02671; 1FZD.
CC DR Genew: HGNC:490; ANGPTL2.
CC DR MIM: 605001; -.
CC DR InterPro: IPR002181; fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C; 1.
CC SMART: SM00186; FBG; 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW signal; Coiled coil; Glycoprotein.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 493 ANGIOPOIETIN-RELATED PROTEIN 2.
CC FT DOMAIN 76 115 COILED COIL (POTENTIAL).
CC FT DOMAIN 152 206 COILED COIL (POTENTIAL).
CC FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 493 AA; 57104 MW; 0F2ADBE353D185CA CRC64;

Query Match 20.0%; Score 400; DB 1; Length 493;
Best Local Similarity 31.9%; Pred. No. 1.5e-24;
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

OY 97 NELMNRVLLTTFVFKQ-----LDPPHPRVOSHGLDCTDIDTIGSVTKTPSG----- 146
DB 231 NRIINQI--STNEIQSDONIKVLPPLPTMPPTLT-----SLPSTDKRSGPMWDC 278
OY 147 -----LYIHREGSSYFEWCDMDYRGGWTVYQKRIIDGIDFORLMCDVLD 194
DB 279 LQALEGDHDTSTIYLVKPEENTNRLMQWCDOHRDPGCVTYIQKRLDSVNFRRMWEYTKQ 338
OY 195 GFQDLLGEFWMGLKTIYVNOKNTSEMLYVALESEDDTLAYASYDNFMLEDETRFFKMH 254
DB 339 GFQNDGEYWLGLENIYVLMQGN--YKLLVTMEDWSGRKVFAYASFLREPESEYKRL 396
OY 255 LGRYSGNAGDAFRGLKKEDNONAMPSTSDVDNDCRPACLVNCGSAKSCSHLNKKGW 314
DB 397 LGRYHGNAGDSFTW-----HNGKQFTTLDRDHD-----VYTG-----NCAH-YQKGMW 439
OY 315 FNNCGLANLINGIHFSKLLA---TGIONGTWTKNNSPVKIKSYSMKIRMPY 366
DB 440 YNCAHSHNLNGWYRGGHYRSRYODGYVAEF--RGGSYSLLKVVMMIRPNPTF 492

RESULT 6
FGL1_HUMAN
ID FGL1_HUMAN STANDARD; PRT; 312 AA.
AC O9UK09;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR AR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;


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DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG_C-DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal; Polymorphism.
FT SIGNAL 1 15
FT CHAIN 16 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
FT VARIANT 269 269
FT MISSING (IN CELL LINE T98G; MAY BE DUE TO EXON SLIPPAGE).
FT /FTID-VAR 009940.
SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match 19.8%; Score 395; DB 1; Length 498;
Best Local Similarity 27.0%; Pred. No. 3,9e-24;
Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

OY 3 VQNCVYHSTDSVNIIVEDGSNAKDESKNDYCKEDSCDYKTKITREKHFRCN 62
DB 115 IQONNAVQNHNT---ATMLEIGTSLISQT-----AEQTRKLTDEVTQVLTNQSRLIEQL 163
OY 63 LQNSIVSY-----
DB 164 LENSLSYKLEKOLLOOTNEILKIHENKSLLEKHKLEMECKHKEELDTLKEEKENLQGLV 223
OY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEYF-----RKOLDPF 118
DB 224 TRQTYIIQELKELKQATNNSTNLSYLOKQOELMOTVHNVLCTKEGVLTKGKRREEKPF 283
OY 119 PRRPVQSHGLDCTDIKDITGTSVTKTPSGLYTIHPREGSSYFEVWCMYDYGCGWTYIQKR 178
DB 284 -----RDCAADV-----QAGFNKSGIYTYIINNPERKKYFCNMVDVNGGWTYIQHR 330
OY 179 IDGIIDFORLMCDYLDGFGDLGEFWLGLKKIFYVNOKRTSMFLYVLALESDDTLAYAS 238
DB 331 EDSGLDFQRGWKRYKMGFGNPSGEYWLGNFEITAITSOR--QYMLRIELMDWEGNRAYSQ 388
OY 239 YDNFWLEDETREFKMLHGRYSNAGDAFRGLKKEDN--QNAPEFSTSDVNDGCRPAC-- 294
DB 389 YRFHIGNKEKQNYRLYLKHTGTAG-----KQSSLLHGADEFSTKADADNDGCMCKCAL 441
OY 295 LVNQGQVSKCSHLNKTGMWFNFCGLANLNGIHNF-----GKLATGIGMGCTWTKNNSPV 350
DB 442 MLTG-----GWMFDCGPSNLMNGMYTAGQNHGKL--NGIKWHYF--KGPSY 484
OY 351 KIKSVSMKIR 360
DB 485 SLRSTTMIR 494

RESULT 9
ACPL_MOUSE STANDARD: PRT: 498 AA.
AC 008538:
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DE 16-OCT-2001 (Rel. 40; Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN ANGPT1 OR AGPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97134663; PubMed=8980223;

```

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RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonneville P.C.,
RA Yancopoulos G.D.,
RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning."
RL Cell 87:1161-1169(1996).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIAL AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED. MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: U83509; AAB50558.1; -.
CC HSP; P02671; IZD.
CC MGI:108448; Agpt.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG_C-DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 19
FT CHAIN 20 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC26D800 CRC64;

Query Match 19.6%; Score 391; DB 1; Length 498;
Best Local Similarity 26.7%; Pred. No. 8,2e-24;
Matches 115; Conservative 67; Mismatches 126; Indels 122; Gaps 16;

OY 3 VQNCVYHSTDSVNIIVEDGSNAKDESKNDYCKEDSCDYKTKITREKHFRCN 62
DB 115 IQONNAVQNHNT---ATMLEIGTSLISQT-----AEQTRKLTDEVTQVLTNQSRLIEQL 163
OY 63 LQNSIVSY-----
DB 164 LENSLSYKLEKOLLOOTNEILKIHENKSLLEKHKLEMECKHKEELDTLKEEKENLQGLV 223
OY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEYF-----RKOLDPF 118
DB 224 TRQTYIIQELKELKQATNNSTNLSYLOKQOELMOTVHNVLCTKEGVLTKGKRREEKPF 283
OY 119 PRRPVQSHGLDCTDIKDITGTSVTKTPSGLYTIHPREGSSYFEVWCMYDYGCGWTYIQKR 178
DB 284 -----RDCAADV-----QAGFNKSGIYTYIINNPERKKYFCNMVDVNGGWTYIQHR 330
OY 179 IDGIIDFORLMCDYLDGFGDLGEFWLGLKKIFYVNOKRTSMFLYVLALESDDTLAYAS 238
DB 331 EDSGLDFQRGWKRYKMGFGNPSGEYWLGNFEITAITSOR--QYMLRIELMDWEGNRAYSQ 388

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OY 239 YDNFWLEDETRFKMHLGRYSNGNDAFRGLKEDN--QNMFPSTSDVNDGCRPAC-- 294
DB 389 YDRFHIGEKONRYLKGHTAG-----KOSLLHGADFTKADNCKCKAL 441
OY 295 LVNGOSVAKSCHLNKGMFNECGIANLNGIHRS---SKLATGIGOMGTWTNNSPV 350
DB 442 MLTG-----GWMFDAGSPSLNMGMYTAQGNHGL--NGIKMHF--KGPSY 484
OY 351 KIKSVSKIR 360
DB 485 SLRSTTMMIR 494
RESULT 10
AGP2_HUMAN STANDARD; PRT; 496 AA.
ID AGP2_HUMAN
AC 015123; Q9NRR7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Masiopiarre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radzilewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RT Science 277:55-60(1997).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=20309815; PubMed=10766762;
RA Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2.";
RL J. Biol. Chem. 275:18550-18556(2000).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF004337; AAB63190.1; -
CC EMBL: AF187658; AAF76526.1; -
CC HSSP: P02671.1.FZD.
CC Genew: HGNC:485; ANGPT2.
CC MIM: 601922; -
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C.1.
CC SMART: SM00186; FBG. 1.

DR PROSITE: PS00514; FIBRINAG_C_DOMAIN: 1.
KW Fibroprotein: Coiled coil; Signal; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 496
FT DOMAIN 130 256
FT DOMAIN 280 496
FT CARBOHD 89 89
FT CARBOHD 119 89
FT CARBOHD 133 133
FT CARBOHD 151 151
FT CARBOHD 240 240
FT CARBOHD 304 304
FT VARSPLIC 97 148
SQ SEQUENCE 496 AA; 56919 MW; 5642A5847A7385C CRC64;
Query Match 19.1%; Score 381.5; DB 1; Length 496;
Best Local Similarity 26.3%; Pred. No. 4,7e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;
OY 3 VQNCVHHSTDSVVNIYEDGSNADESKSDTYCKEDCEESCDVYKTI---TREE--- 55
DB 112 IQONAVONOT---AVMIEIGTLNLT---AEQTRKILTYEAGVLNQTRELEQL 160
OY 56 -KHFRCRN-LQNSIYSYRSTKLL-----LRNMDDQASL 89
DB 161 LEHSLSTNKLKQLIDQYSEINKLQDKNSFLKKVLAEMDKHIIQLQSTKEEDQLQVLY 220
OY 90 DYLSQVNEELMNRVLLLT--TEVFRKQ-----LDPPHPRVQSH 126
DB 221 SKQNSIIELEKKIYATVYNNVSLQKQHDMEYNNLLTMSTNSAKDPVAKEDQIS 280
OY 127 GIDCTDIDKDTGSVYKTPSGLYIHPGSSYFEVCMQDYGGMVYIQKRIDIDFQ 186
DB 281 FPDCAFEVRS---GHTNGIYTLTFPNSTEIRKAYCDMEAGCGMTIIQRREDSVDFQ 336
OY 187 RLMCYLDGFGDLGEPFMGLKKIFYIYNQKNTSMVLVALESEDDTLAYSYDNFWLED 246
DB 337 RFWKEYKVGFGSPSEYVGNFVSQLTNQQR--YVLKHLMDGNEVSYLSEHYFLSS 394
OY 247 ETRFFKMLHGRYSNGNDAFRGLKEDNQNAMPFSTSDVNDGCRPACLVNGOSVAKSCH 306
DB 395 EELANRHLHKLGTGRKRI-----SSISQPGNDFSTKQDNCK-----ICKSQ 439
OY 307 LHNKGMFNECGIANLNGIH---FSGLATGIGOMGTWTNNSPVKIKSVSKIR 360
DB 440 MLT-GWMFDAGSPSLNMGMYTPQRONTNKF--NGIKMYW--KSGSYSLKATYMMIR 492
RESULT 11
FIBB_HUMAN STANDARD; PRT; 491 AA.
ID FIBB_HUMAN
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen.";
RN Adv. Exp. Med. Biol. 281:39-48(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M.Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic

RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
 RL Biochemistry 22:3244-3250(1983).
 [13]
 RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 fibrinogen.";
 RL (in) Liu C.Y., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 [14]
 RP SEQUENCE FROM N.A., AND VARIANTS SRR-100; HIS-170; LEU-265 AND
 RP LYS-478.
 RA Riederer M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 [15]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Soutlan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 structural variants.";
 RL (in) Peeters H. (eds.);
 RL Profiles of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 [16]
 RP SEQUENCE OF 31-491.
 RX MEDLINE-79124640; Pubmed-420779;
 RA Watt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 [17]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE-7625080; Pubmed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 [18]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE-87146483; Pubmed-3029722;
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 [19]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 [110]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE-83254370; Pubmed-6575689;
 RA Henschen A., Lottspeich F., Kehl M., Soutlan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 [111]
 RP DISULFIDE BONDS.
 RX MEDLINE-77245999; Pubmed-891553;
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 [112]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neutra H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 [113]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE-84305751; Pubmed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 [114]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE-97472408; Pubmed-933323;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 [115]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE-98292395; Pubmed-9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 [116]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-99175089; Pubmed-10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 [117]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE-89058942; Pubmed-3194892;
 RA Schmelzer C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RT structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 [118]
 RP VARIANT ISE.
 RX MEDLINE-91208409; Pubmed-2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RT replacement of B beta glycyl-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 [119]
 RP VARIANT NAPLES.
 RX MEDLINE-92340664; Pubmed-1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta
 RT 68 Ala-->Phe.";
 RL J. Clin. Invest. 90:238-244(1992).
 [120]
 RP VARIANTS JUMUIDEN AND NIJMEGEN.
 RX MEDLINE-92228809; Pubmed-1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Noyakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens Jumuiden (B beta Arg14-->Cys) and Nijmegen (B
 RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 [121]
 RP VARIANT NEW YORK-1.
 RX MEDLINE-85157605; Pubmed-3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 [122]
 RP FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 RP POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 RP AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE

RT "Cloning of the complete coding sequence of rat fibrinogen B beta
RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary
RT structure.";
RL Blood Coagul. Fibrinolysis 5:487-496(1994).
RP
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowles D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
RN
RN SEQUENCE OF 19-32.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN
RN SEQUENCE OF 183-479 FROM N.A.
RX MEDLINE=89378771; PubMed=2673932;
RA Eastman E.M., Galula N.B.;
RT "Cloning and characterization of a cDNA for the B beta chain of rat
RT fibrinogen: evolutionary conservation of translated and
RT 3'-untranslated sequences.";
RL Gene 79:151-158(1989).
RN
RN SEQUENCE OF 425-479 FROM N.A.
RC STRAIN=WiStar; TISSUE=Liver;
RX MEDLINE=87134033; PubMed=3817019;
RA Soczek J., Lotli A.-M., Taroux P., Duguet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
RT liver regeneration.";
RL Exp. Cell Res. 169:47-56(1987).
CC
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
CC
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CC
CC -----
DR EMBL: U05675; AAA64866.1; -
DR EMBL: M27220; AAA41160.1; -
DR EMBL: K01336; AAA98625.1; -
DR EMBL: M35602; AAA41159.1; -
DR PIR: A05299; A05299.
DR PIR: PE0010; PE0010.
DR HSSP: P02675; 1EZE.
DR InterPro: IPR002181; Fibrinogen.C.
DR Pfam: PF00147; fibrinogen.C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG-C-DOMAIN; 1.
KW Blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 219 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 219 304 (BY SIMILARITY).
FT DISULFID 229 258 (BY SIMILARITY).
FT DISULFID 412 425 (BY SIMILARITY).
FT DISULFID 412 425 (BY SIMILARITY).

FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
FT CONFLICT 439 439 L -> O (IN REF. 5).
FT CONFLICT 441 441 S -> T (IN REF. 5).
FT CONFLICT 445 445 S -> A (IN REF. 5).
FT CONFLICT 467 467 R -> K (IN REF. 5).
FT CONFLICT 475 475 V -> F (IN REF. 5).
SQ SEQUENCE 479 AA; 54303 MM; EC8C6DB77C3BEDEC0 CRC64;

Query Match 18.7%; Score 373.5; DB 1; Length 479;
Best Local Similarity 27.2%; Pred. No. 1.9e-22;
Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;

QY 5 GNCVHNSTSSVNVNLYEDGSNAKDESKSNDYCKEDCESGVKRTITEEKHFQNRNQ 64
DB 81 GGCYVHGGDMGVL-----CATGCELRQTLNHE-----RPIK 112
QY 65 NSIV-----SYTRSTKLLRNMDQOASLDYLSNOVE----- 98
DB 113 NSIAELNSINSVYESSVTFQYLTLTKDMKKKQAVQNDENVINEYSIEDQKLYD 172
QY 99 -----LMNRVLLTTEVFRKQLD-----PPRPVQSH-----GLDCYDI 133
DB 173 ETVNDNIPRLNRLVLSILEDLSRKMKQLESISAQTEYCHTPTVCNIPVYSGKECEI 232
QY 134 KPTISVTKPSGLVYIHPGSSYPFVNCDDYRGCGFTVQKRDIIDFQRLMCDL 193
DB 233 IRRGERT-----SEMYLDQDTSSKPRVYCDMKTEGNGVTIOMQDGSVDEGRWMDPK 288
QY 194 DFGGD-----LLGEFVLGLKIFYIVNOKNTSFMLYVALSEDDTLAVASYDN 241
DB 289 KFGNATNEDTKKYCGLDGEYWLGNDRKISQTLRGPTF--LLIEEDMKGKVAHYHG 346
QY 242 FVLEDETRFEKMLHGRYSGNADAF---RGLKEDN---ONAMPFSTDVNDGCRPA 293
DB 347 FTVQTEANKYQVSVKYYKKTACNALMEGASQLVGENRTWTINHGFEFFSYDRDNG---- 402
QY 294 CLVNGQSVSGHLNKGWMEFEGLANLNGIHHSGL-----LATIGCTWTK 345
DB 403 -WYTTDPRKQCK-EDGGGMYNRCNANPNRYYWGLYSWMSKHGTTDGVVMMW-- 458
QY 346 NNSPVKIKSVSKIRMY 363
DB 459 KGSWSMRMSMKIRPVF 476

RESULT 15
FIBG_HUMAN
ID FIBG_HUMAN STANDARD: PRJ: 453 AA.
AC P02679; P04469; P04470; Q96KJ3; Q96A14;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen gamma chain precursor (PRO2061).
GN FGG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
RX MEDLINE=85252774; PubMed=2990550;
RA Rixon M.W., Chung D.W., Davie E.W.;
RT "Nucleotide sequence of the gene for the gamma chain of human
RT fibrinogen.";
RL Biochemistry 24:2077-2086(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283434; PubMed=6688357;
RA Chung D.W., Chan W.-Y., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the gamma chain of human fibrinogen.";
RL Biochemistry 22:3250-3256(1983).

- [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A AND GAMMA-B).
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC TISSUE-Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC TISSUE-Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 27-437.
 RA Henschen A., Iottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants."
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [7]
 RP SEQUENCE OF 75-286 FROM N.A.
 RC TISSUE-liver;
 RA MEDLINE-92119334; PubMed-1685103;
 RA Marchetti L., Zaneli T., Malcovati M., Tencchini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene."
 RL DNA Seq. 1:419-422(1991).
 RN [8]
 RP SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA MEDLINE-85030379; PubMed-6092346;
 RA Fornace A.J. Jr., Cummings D.E., Cant J.A.,
 RA Crabtree G.R.;
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen."
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [9]
 RP SEQUENCE OF 209-270 FROM N.A.
 RA MEDLINE-84069777; PubMed-6689067;
 RA Inam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma chains of human fibrinogen."
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RP SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
 RA MEDLINE-82068993; PubMed-7306501;
 RA Wolfenstein-Todel C., Moseson M.W.;
 RT "Carboxy-terminal amino acid sequence of a human fibrinogen
 RT gamma-chain variant (gamma')."
 RL Biochemistry 20:6146-6149(1981).
 RN [11]
 RP REVIEW, AND DISULFIDE BONDS.
 RA Henschen A., Iottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen."
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.W., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin."
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RP DISULFIDE BONDS.
- RX MEDLINE-76225080; PubMed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen."
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE-83231465; PubMed-6860649;
 RA Hoepflich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation."
 RL Biochemistry 22:2049-2055(1983).
 RN [15]
 RP SULFATION.
 RX MEDLINE-91369960; PubMed-1892842;
 RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
 RT "Recombinant human fibrinogen and sulfation of the gamma' chain."
 RL Biochemistry 30:9414-9420(1991).
 RN [16]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE-84305751; PubMed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin."
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [17]
 RP POLYMERIZATION SITE.
 RX MEDLINE-85014892; PubMed-6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [18]
 RP POLYMERIZATION SITE.
 RX MEDLINE-81142375; PubMed-6451630;
 RA Oleksa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site."
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [19]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84203545; PubMed-6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain."
 RL Biochemistry 23:1767-1774(1984).
 RN [20]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84185664; PubMed-6325435;
 RA Plov E.F., Strouj A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets."
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [21]
 RP CALCIUM-BINDING SITE.
 RX MEDLINE-85261382; PubMed-3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by terbium fluorescence."
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [22]
 RP CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
 RX MEDLINE-81054908; PubMed-6933547;
 RA Wolfenstein-Todel C., Moseson M.W.;
 RT "Human plasma fibrinogen heterogeneity: evidence for an extended
 RT carboxyl-terminal sequence in a normal gamma chain variant
 RT (gamma')."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE-97169449; PubMed-9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., Le Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen."

RL Structure 5:125-138(1997).
RN [24]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RX MEDLINE=97352771; PubMed=9207064;
RA Pratt K.P., Cole H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
RT "The primary fibrin polymerization pocket: three-dimensional
RT structure of a 30-kDa C-terminal gamma chain fragment complexed with
RT the peptide Gly-Pro-Arg-Pro.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
RN [25]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RT crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [26]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [27]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RT
Query Match 18.6%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 2,6e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
QY 65 NSIVSTNSTKRLNNMDEQ-----QASLDYLSNQVNELMNRVLLTTEVFRKQDPF 118
DB 103 NMIDATILKSRMLEIMKYEASILTHDSIRYLOEIYNSNNQKIVNLKEV--AQLEAQ 160
QY 119 PHRP-----VQSH---GLDQTDIKDTIGSVTKTPSGIXIHPGSSYFEVMCDMDYRGSG 171
DB 161 COEPCKDVQIHDTGKDCQD---IANKGAKQSGLYFTKPLKANQOFLVCEIDSGNG 216
QY 172 WTVIQKRIDGIDFQRLMCDYLDGFGDL---LGEEFWLGKIKFYIVNQKNTSFMLYVAL 227
DB 217 WTVFQKRIDGSDVFKKNWLYQKEFGHLSPTGTEFWLQNEKIHLSIQSAIPYALVEL 276
QY 228 ESEDDTLAYASTDNFWLEDETFEPKMHILGRYS-GNAGDAFRGLKKED-----NQNAM 278
DB 277 EDWNGRTSTADYAMFKVGEADKRYRLTYAVYFAGGDADAFDGFEDDPSDKFTSHNGM 336
QY 279 PESTDVDNDGCRPACLVNGQSVKSGSHLNKTKGMWNEGGLANLGIHHSGL----- 333
DB 337 QPSTWDNDNDKFEKNCDAEDGS-----GWMNKCCHAGHLNGVYVGQGYSKAST 385
QY 334 --LATGIQMGWTNRKNSPVKIKSVSMKI 359
DB 386 PNGYDNGIIMATW--KTRWYSMKKTTMKI 412

Search completed: December 16, 2002, 17:34:41
Job time : 10.7619 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:08 ; Search time 27.746 Seconds
(Without alignments)
2732.835 Million cell updates/sec

Title: US-09-596-196-9

Sequence: 1 EVVQNCVHHSTDSVVNIY.....PVKIKSVSMKIRRMYPYFK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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1: SP_RHIZOBL_21: *
2: 1: sp. archaea: *
3: 2: sp. bacteria: *
4: 3: sp. fungi: *
5: 4: sp. human: *
6: 5: sp. invertebrate: *
7: 6: sp. mammal: *
8: 7: sp. mhc: *
9: 8: sp. organelle: *
10: 9: sp. phage: *
11: 10: sp. plant: *
12: 11: sp. rodent: *
13: 12: sp. virus: *
14: 13: sp. unclassified: *
15: 14: sp. virus: *
16: 15: sp. r_virus: *
17: 16: sp. archaeap: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	427.5	21.4	652	5	Q9NDQ1	Q9ndq1 ciona intes
2	425	21.2	451	4	Q95841	Q95841 homo sapien
3	409.5	20.5	357	11	Q9EP17	Q9ep17 rattus norv
4	404.5	20.2	493	11	Q9J0J3	Q9j0j3 rattus norv
5	399.5	20.0	489	13	Q90Z18	Q90z18 brachydanil
6	390	19.5	498	6	Q9ND48	Q9nd48 sus scrofa
7	382	19.1	495	4	Q9EPY7	Q9epy7 homo sapien
8	379.5	19.0	346	4	Q45827	Q45827 homo sapien
9	379.5	19.0	456	11	Q9D2D2	Q9d2d2 mus musculi
10	378.5	18.9	407	13	Q9DER1	Q9der1 gallus gae
11	378.5	18.9	488	13	Q91589	Q91589 xenopus lae
12	378.5	18.9	493	13	Q9DER2	Q9der2 gallus gall
13	376.5	18.8	441	13	Q9DER0	Q9der0 gallus gall
14	375	18.8	308	5	Q9U8W6	Q9u8w6 tachypleus
15	373.5	18.7	496	6	Q9EDY7	Q9edy7 sus scrofa
16	370	18.5	316	5	Q9U8W7	Q9u8w7 tachypleus

17	369.5	18.5	220	5	08T8A2	08T8A2 ciona savig
18	368.5	18.4	407	13	09P054	09P054 gallus gall
19	368.5	18.4	436	4	08W0R3	08W0R3 homo sapien
20	368.5	18.4	436	11	08VCW7	08VCW7 mus musculu
21	368	18.4	314	11	08VC25	08VC25 mus musculu
22	367.5	18.4	337	6	08RIO3	08RIO3 mus musculu
23	364.5	18.2	431	6	095L03	095L03 macaca fasc
24	364.5	18.2	513	13	090Z19	090Z19 brachydanio
25	359	17.9	244	4	09HBP3	09HBP3 homo sapien
26	359	17.9	341	5	0966W1	0966W1 homo sapien
27	358	17.9	435	13	093568	093568 gallus gall
28	357.5	17.9	932	13	057587	057587 brachydanio
29	354	17.7	356	5	095P98	095P98 halocynthia
30	352.5	17.6	592	4	095697	095697 homo sapien
31	352.5	17.6	1294	4	09U0P3	09U0P3 homo sapien
32	352	17.6	324	5	095PA0	095PA0 halocynthia
33	348	17.4	292	5	09U8W8	09U8W8 tachyleus
34	347	17.3	324	5	095P99	095P99 halocynthia
35	341	17.1	316	6	028529	028529 mustela put
36	339	17.0	712	4	000531	000531 homo sapien
37	339	17.0	1358	4	092752	092752 homo sapien
38	339	17.0	015568	4	015568	015568 homo sapien
39	333.5	16.7	372	5	018545	018545 biomalhari
40	333.5	16.7	385	5	095U99	095U99 biomalhari
41	332.5	16.6	337	6	095E00	095E00 macaca fasc
42	330	16.5	1356	11	005546	005546 rattus norv
43	327.5	16.4	235	6	028763	028763 papio cynoc
44	327.5	16.4	1353	13	000566	000566 gallus gall
45	321.5	16.1	440	5	09W291	09W291 drosophila

ALIGNMENTS

RESULT 1

AC	09ND01;	PRELIMINARY;	PRT;	652 AA.
AD	09ND01;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Fibrinogen-like protein.			
GN	CI-FIBRN.			
OS	Ciona intestinalis.			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;			
OC	Phlebobranchia; Clonidae; Ciona.			
OX	NCBI_TaxID=7719;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hotta K., Takamashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,			
RA	Satcho N.;			
RT	"Characterization of Brachyury downstream notochord genes in the Ciona			
RT	intestinalis embryo.";			
RL	Submitted (JAN-2000) to the EMBL/Genbank/DBSJ databases.			
RL	EMBL; AB036849; BAB00626.1; -.			
DR	HSSP; P02671; LFZD.			
DR	InterPro; IPR002181; Fibrinogen_C.			
DR	Pfam; PF00147; fibrinogen_C. 1.			
DR	SMART; SM00186; FRG; 1.			
DR	PROSITE; PS00514; FIBRN_AG_C_DOMAIN; 1.			
QO	SEQUENCE 652 AA; 73252 MW; A492BA25162P0E0 CRC64;			

Query Match	21.48;	Score 427.5;	DB 5,	Length 652;
Best Local Similarity	30.78;	Pred. No. 6.7e-27;		
Matches 115; Conservative	67;	Mismatches 124;	Indels 69;	Gaps 16

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OY 30 SKSDNYCK---EPCSECDVKTRTREKHFH-----CNLONSITYSYRS-----73
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 293 SQENDDAKAEABDVTRVETTDRTVCEQYVTEDEQVETSTTRSQVTSRSRBYTHENN 35
OY 74 ----TKLLRMNMBQOASL-----DYSNOVN--ELMNRVLLLTTEVPKOL 115
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 353 EAMFSTVTHAVEVTOQNYLYSESGVNIIDQVATNTEGIEFTSLRLAT-----404

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QY	116	DPFHRRQSHGL--DCDDIDITIGSYTKPRPSCGYIIHPRESSYPEFVMDMORYGGWT	173
Db	405	NPTFVQDQGTSLSYDDCAEL-----AGVROSQGYIDRP-GTKWTIVYUCMDIDGGGWT	459
QY	174	VIQRIDGIIIDFQRLMCDYLDGFDLLGEFWLGLKLFYI-VNOKNTSPMLYALSESDD	232
Db	460	MLQRRIGIVFSGWMSYKNGFEDINADHIGLEKMHISTSKSRMRRLITLTDMD	519
QY	233	TLAASYDNFMLEDETREPKHHLGRYSNGNDARGLKLEEDNOAMBEFTSDVNDQCRP	292
Db	520	VSHANTGVFIRSEGGKYQOLAKRYITGTADAL-NGENYNNHLOPFTTPDRND---	574
QY	293	ACLVNGOSVKSCHLHNKTGMWNECGLANLNGITHPESG--KLATGICGWTWK-----	345
Db	575	-----GYALGNCGRYV-RSGWMFNAFCAANLNG-NYTTGPKYQGNQIYGTWTYKLDST	627
QY	346	NNSPVKIKISVSMKTR 360	
Db	628	SNSRYSFERYDMKVR 642	

RESULT 2			
095841			
ID	095841	PRELIMINARY;	PRT; 491 AA.
AC	095841;		
DT	01-MAY-1999 (TrEMBLrel. 10, Created)		
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	Angiopoletin Y1 (DU595C2.2) (Angiopoletin-related protein 1 precursor).		
DE	precursor).		
GN	DU595C2.2 OR ARP1.		
OS	homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEART;		
RC	MEDLINE=9914829; PubMed=10025962;		
RA	Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;		
RT	"Molecular cloning and characterization of a novel angiopoietin family		
RL	protein, angiopoietin-3.,"		
RL	FEBS Lett. 443:353-356(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Cobley V.;		
RL	Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RC	Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,		
RA	Yamamoto J., Sugano S., Isogai T.;		
RT	"hRI human cDNA sequencing project.,"		
RL	Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.		
RL	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RC	Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,		
RA	Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuo Y.,		
RA	Suda T.;		
RT	"Molecular cloning and characterization of novel angiopoietin-related		
RT	protein (ARP4).,"		
RL	Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.		
RL	[5]		
RP	EMBL; AF107253; AAD19608.1; -		
DR	EMBL; AL355520; CAC13169.1; -		
DR	EMBL; AB056476; BAB40691.1; -		
DR	HSSP; P02671; 1FZD.		
DR	InterPro: IPR002181; Fibriogen_C.		
DR	Pfam: PF00147; Fibriogen_C.1		
DR	SMART: SM00186; FBG; 1.		
DR	PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.		
DR	Signal.		
DR	Signal.		

FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	491	POTENTIAL.
SO	SEQUENCE	491 AA;	56719 MM;	3CADB8DEF6C7E99 CRC64;
	Query Match	21.2%;	Score 425;	DB 4; Length 491;
	Best Local Similarity	26.9%;	Pred. No. 7.4e-27;	
	Matches 119;	Conservative 64;	Mismatches 133;	Indels 126; Gaps 14.
OY	24	SNADKESNSDVTCKEDCEESCDVYTKITRE-EKHMCNRLONSIVSYSTRSKLLRNMM	82	
Db	68	TKGQASTYTKIMITPMDELNLEKDYLSRQREIDVQLVVDVGNINVEYKLLRKESRNMM	127	
OY	83	DE-QQASIDYL-----SNQVIELMRYLLTTE-----	109	
Db	128	SRVTLQYMLLEHETIRKRDNSLELSOLEKKNILVNTTEMKATRYRELEVKYASTLTDLVN	187	
OY	110	-----VFRKQ--LDP-----FPHRPVQSHG-----	128	
Db	188	NOSVMITLLEBQCLAFISNRDTHNVPRLVQVYRPHNPNQVTPBGLIGNETIQDRPGYPR	247	
OY	129	DCTDIKDTIGSVTKPR-----SGLYIIRPGESSVPEV	161	
Db	248	DLMPRPDLATSPETKSPFKIPVTFINEGPFKDCQQAKEAGHSVSGVIMIKPEPNSGMQL	307	
OY	162	MCDMMYRGGGWYIQRKRIDGIIDFQRLMCDYLDGSGDLGEEWLGKATFTYVYNQNTSF	221	
Db	308	WCENSLDPGGWYIQRKRIDGSVNFPRMNMENYKKGSGINDGEWLTGENTYIMLSNDN--Y	365	
OY	222	MLYVALSEEDDTLAAASYDNFWLDEDETREFKHLIRYSGNACDAFRLGKKEDNONAMPSS	281	
Db	366	KLLIELEDMSSDKKYAAEYSSFRLEPESEYRIKRLTGYQGNACDSSMM-----HNGKQFT	419	
OY	282	TSDVDNDCRPACLVNGGSVKSCHLHNKGTGMFNECGLANGINHFSGLLA--TGI	338	
Db	420	TLDRLDKD-----MYAGNCALFH--KGMWYNAACASNLNGWYRGCHYRSKHQDGI	468	
OY	339	OMGTWTKNNSPYKIKYSVMKTR	360	
Db	469	FMAEY--RGGSYSLRAYQMMIR	488	

```

RESULT 3
09EPT7
ID 09EPT7 PRELIMINARY; PRF: 357 AA.
AC 09EPT7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Prothrombinase FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC RYCHLIN-SPRAGUE-DAWLEY;
RA RYCHLIN D.F., Chlen E., Philippe M.;
RT "FGL2 Expression in the Sprague-Dawley Rat. ";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF323608; AAG42269.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31183DD9A02EBBA9 CXC64;

Query Match 20.5%; Score 409.5; DB 11; Length 357;
Best Local Similarity 32.0%; Pred. No. 9.3e-26;
Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;

16 VNIINIDGSGNKKDEKSDNTVCKEEDCERSCDV--KTKITREKHFMCMCNLAQNSIVSYSTRS 73

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Db 4 VLKEVFTLQEAVDLSLKKSCQDCKLQADEHPDPCNGAETAEAD-----NRVQLESQVKN 57
Oy 74 TKLLRNMADEOQA-----SL-----DYLNSQVNEIMNRVLLTTEVER----- 112
Db 58 LSELKNAKEEIIQLOGRLLESJLQVMMNNIENTVDNKNVNLTVSVNSLDSKCKPCSOEH 117
Oy 113 KOLDPPHAPVOSHGLDCDIDIKDTIGSVTKPSGLYIIHEGSSYPPEVNCMDYRGCGW 172
Db 118 NQDPNPOVHILYK-----DCSDYV-VLG---KRSSGTYRVMPDHRNSPEYVCDMETTGGW 169
Oy 173 TVYQKRIIDIDFQRLMCTYLDGFGDLGFEFNLGKKIFIVNQKNTSFMLYALSEDD 232
Db 170 TVYQARLDSTFTNMGKMYKAGFNLEREFWLGNDKIHLLT--KSKEMILRIDLEDGNG 227
Oy 233 TLAYASVDNFWLEDETRFFRMHLGRYSNGNADAFRLGKKEDENONAMPFSTDVNDGCRP 292
Db 228 LTLIYAVYDQFYANEFKLRLHGNNGTRAGDLR-FSRINYNDLRFETTPDRDNDRYPS 286
Oy 293 ACLVNGQSVKSCSHLNKGTGWFNFCGLANLNGIH--FSGRLATGIGWGTM--TRKN 347
Db 287 G-----NCG-LYSSGWFMDACLSTANLNGKYNNQRYKG--VRNGIFMGWTPGVSOA 334
Oy 348 SPYKIKSVSKIRRMATNP 365
Db 335 HPGYKFSFKAKMMLNP 352

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RESULT 4

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Oy 09J03 PRELIMINARY; PRT; 493 AA.
ID 09J03
AC 09J03;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Angiotensin II type 1A receptor associated protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR-KYOTO; TISSUE=VASCULAR SMOOTH MUSCLE;
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Adi-Daoude E., Orlov S.N.,
RA Inagami T.;
RT "ARAP1 is required for recycling and resensitization of angiotensin II
RT type 1A receptor.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF159043; AAF80364.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Receptor.
SQ SEQUENCE 493 AA; 57159 MW; 7C37652C472B2341 CRC64;

```

Query Match 20.2%; Score 404.5; DB 11; Length 493;

Best local Similarity 27.1%; Pred. No. 3,7e-25;

Matches 108; Conservative 68; Mismatches 118; Indels 105; Gaps 15;

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Oy 42 EESCDVTKIT-----REEKHFMCRLQNSIVSYSTRKILRNMADEOQ--A 87
Db 125 KESRRNMSRVTLQYMLLHEIRKRDNALDELQLENILNOTADMQLVSKYKDLKHKFQ 184
Oy 88 SLDYLSQVNEIM-----NRVL--LITTEVER 112
Db 185 HLDMLAHNOSEVIAQLAEHCQRYPARVPQPPATPPRYVQPTVYKRIINQISTNEIOS 244
Oy 113 KO-----LDP-FPIRPVOSHGLDCTIDKDTIGSVTKTPSG-----LYII 150
Db 245 DQMLKVLFPFLPTMPALT-----SLPSSIDKPSGFWRCQLALBEGHSTSSITLV 294
Oy 151 HPGSSYPPEVNCMDYRGCGWTVIQRIDGIIDFQRLMCTYLDGFGDLGFEFNLGKKI 210

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Db 295 KPEPTNLMQVWCQDQRDPGQWTVIQRRLDGSVAFEFNMTWYKQGFENIGCEYWLGIENI 354
Oy 211 FYIVNQKNTSFMLYVALESDDTLAYASYDNFMFLEDETRFKNHILGRYSNAGDAFGLK 270
Db 355 YMLTNQGN--YKLLVTMEDNSGRKRVFAETVASFLEPESEYTKLALGTVHGNAGDSTFW-- 410
Oy 271 KEDNONAMPFSTDVNDGCRPACTLVNGQSVKSCSHLNKGTGWFNFCGLANLNGIHFS 330
Db 411 -----HNGKQFTITDROHD-----YITG-----NCAH-YQKGGWYVNCALSNLNGVYRG 455
Oy 331 GKLLA--TGIGWGTWKNNSPYKIKSVSKIRRMATNP 366
Db 456 GHYRSRYQDGVYMAEF--RCGSYSLKRVVMIRPNPTVF 492

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RESULT 5

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Oy 090218 PRELIMINARY; PRT; 489 AA.
ID 090218
AC 090218;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Angiopoietin-2.
GN ANG2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21391693; PubMed-11500985;
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiopoietin
RT genes.";
RL Dev. Dyn. 221:470-474(2001).
DR EMBL; AF379603; AAK83348.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; UNKNOWN.1.
SQ SEQUENCE 489 AA; 55785 MW; 3ABAB6278539B33C CRC64;

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Query Match 20.0%; Score 399.5; DB 13; Length 489;

Best local Similarity 28.1%; Pred. No. 9.4e-25;

Matches 114; Conservative 55; Mismatches 131; Indels 105; Gaps 16;

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Oy 3 VQNCVHSHSDSSVNVIVEDGSSNAKDESKSNDYCKEDCESDVKTKITREEKHFMCRN 62
Db 107 MERNVHTQT-----ATMLEIGTNLLSQSAEN--TCK-----LTDVETQVNLQTS-----R 150
Oy 63 LQNSIVSYSTRKILRNMD-----EQQA 87
Db 151 LEIQLESLSTNRLERKOLETOEVSRLNDKNSYMDQRFADMEAKHSRELQALQOEQQ 210
Oy 88 SLDYLSQVNEIM-----RVLLTTEVERKQDDEPPH-----RPVQS 125
Db 211 LLELLDQ--NELVSYLLEGELASTRNSTLQROQASLTDYQQLLAWTHONDISTPDK 269
Oy 126 HGL--DCTDI-KDTIGSVTKPSGLYIIHEGSSYPPEVNCMDYRGCGWTVIQRIDG 181
Db 270 EMLKFRCAELFKSGV-----TENGIVSIHLRPNSTOKIKVPCDKMKTGGGWTVOHRYDG 324
Oy 182 IIDFQRLMCTYLDGFGDLGFEFNLGKKIFIVNQKNTSFMLYALSEDDTLAYASIDN 241
Db 325 SVDFNRQMDNDKFLGFGDPSGEHWLGNDVILHTTKD--YTLQVLADEHQAISQVDT 382
Oy 242 FWLEDETRFKNHILGRYSNAGDAFRLGKKEDENONAMPFSTDVNDGCRPACTLVNGQSV 301
Db 383 FYIDGEDKKTSLHARGSTAGRT-----SSLTSHSGQFSTKDDQNDQC----- 426
Oy 302 KSCSHLNKTK-GWPFNECGLANLNGIHNF--SGKLATGIGWGTM 343

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Db 427 -SCKCAOMATGSMWFACGSPNLNGIYYSGNSVIRYNSIKMYW 470

RESULT 6

Q9BDY8 PRELIMINARY; PRT; 498 AA.

AC Q9BDY8; ID Q9BDY8; DB 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)

OS Angiopoietin 1.

OC Sus scrofa (Pig).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

NCBI_TaxID=9623;

RP [1]

SEQUENCE FROM N.A.

RA MEDLINE=21153163; PubMed=11230987;

RT "The angiotensin-II/2 system in coronary artery endothelium prevents oxidized low-density lipoprotein-induced apoptosis."

RL Cardiovasc. Res. 49:872-881(2001).

DR EMBL; AF233227; AAK14992.1; .

DR HSSP; P02671; 1F2D.

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

SQ SEQUENCE 498 AA; 57413 MW; ABCIC8EF56061876 CRC64;

Query Match 19.5%; Score 390; DB 6; Length 498;

Best Local Similarity 26.7%; Pred. No. 5,9e-24;

Matches 115; Conservative 66; Mismatches 127; Indels 122; Gaps 16;

QY 3 VQNCVHSTDSVNVIVEDGSNADESKNDTVCKEDCEESCDVTKITREKHFRCN 62

Db 115 IQQNAVQNT---ATMLEIGTSLSQT-----AEQTRKLDVETQVQLNQTSLRLEQL 163

QY 63 LQNGIVSY-----TRSKTKLLRNMM 82

Db 164 LENSISTYKLEKQLIQOTNEILIKHEKNSLLEKILMEGKHELDLTLEKEKNLGLV 223

QY 83 DEQASLDYLSQNVN-----ELM-----NRVLLTTEVF-----RKQLDPF 118

Db 224 TRQYIIIELEKQLNRAITNNVSLQKQLELMDYVHNVLNCTKKGVLKGGKKEVAF 283

QY 119 PHRPVQSHGLDCTDIKDTIGSVTKTPSGLYIIHPREGSSYPFEVMDMDYRGCGWTVIOKR 178

Db 284 -----RCADAVY-----QAGFNKSGIYTYIINNMPERKVFQCNMDLNGSGWTVIOHR 330

QY 179 IDGIIDFQRLMDYLDGFDGLGEFWLGLKKEFYLVNOKNTSFMLYVALSEDDTLAYAS 238

Db 331 EDGSLDFPRGMKEYKMGFGNPSGETWLGNEFLFALTISQ--QYTLRTLEMDWEGNRASQ 388

QY 239 YDNFWLEDETRFEFKMHLGRYSGNAGDAFRGLKEDN--QNAPEFSTDVNDGCRPAC-- 294

Db 389 YDRFLIGNEKQNYRLXLGHSSTAG-----KQSSLLIHGADFSTKADNDNCMKCAL 441

QY 295 LVNGOSVASCCHLHNTKGMWFNEGCLANLNGIHFS-----GKLATGTQMGWTVTRNNSPV 350

Db 442 MLTG-----GWMFEDACGSPNLNGWFTYAGNHGKL--NGIKMYHF--KGPSY 484

QY 351 KIKSVSMKIR 360

Db 485 SLRSTTMIR 494

RESULT 7

Q9P2Y7 PRELIMINARY; PRT; 495 AA.

AC Q9P2Y7; ID Q9P2Y7; DB 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Angiopoietin-2.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP [1]

SEQUENCE FROM N.A.

RA MEDLINE=99126459; PubMed=9927494;

RT Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K., Wands J.R.;

RT "Biologic significance of angiopoietin-2 expression in human hepatocellular carcinoma."

RL J. Clin. Invest. 103:341-345(1999).

DR EMBL; AB009865; BAA95590.1; .

DR HSSP; P02671; 1F2D.

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;

Query Match 19.1%; Score 382; DB 4; Length 495;

Best Local Similarity 26.4%; Pred. No. 2,7e-23;

Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

QY 3 VQNCVHSTDSVNVIVEDGSNADESKNDTVCKEDCEESCDVTKIT---TREE--- 55

Db 112 IQQNAVQNT---AVMIEGTLNLTQ-----AEQTRKLDVETQVQLNQTSLRLEQL 160

QY 56 -RHEKRN-LQNSIYSYTSSTKL-----LRNMDEQASL 89

Db 161 LEHSLSTNLEKQLIDQITSEINKLQDKNSFLKRYLAMEDKHIIQLQSTKEKDDQLQVLY 220

QY 90 DYLSQNVNLEMRVLLLT--TEVFRKQ-----LDPEPHRPVQSHG 127

Db 221 SKQNSIIELEKKIYATATVNNVSLQKQHDLMETVNNLLTMSTSKSDPYTAKEQISF 280

QY 128 LDCTDIKDTIGSVTKTPSGLYIIHPREGSSYPFEVMDMDYRGCGWTVIOKRIDGIIDFQR 187

Db 281 RDCAEFVKS-----GHTNGIVTLTPPNSTEEIKAVCDMEAGGSGWTVIOHRDEGSDVFOR 336

QY 188 LWCDDYLDGFDGLGEFWLGLKKEFYLVNOKNTSFMLYVALSEDDTLAYASDNDWLEDE 247

Db 337 TYKEKTVGFGNPSGETWLGNEFLFALTISQ--YVAKLHLKMEGNEAVSLKEHYLSE 394

QY 248 TRFEFKMHLGRYSGNAGDAFRGLKEDNQNAMPFSTSDVDNDGCRPACLVAGQSVKSCSHL 307

Db 395 ELNRYRIHLKGLGTGKI-----SSISQPGNDFSTRKDGNDKC-----ICKCSQM 439

QY 308 HAKTGMWNEGCLANLNGIH-----FSGKLATGTQMGWTVTRNNSPVKIKSVSMKIR 360

Db 440 LP--GGWMEFACGSPNLNGWYTPORONTNF--NGIKMYW--KSGYSLKATYTMIR 491

RESULT 8

Q43827 PRELIMINARY; PRT; 346 AA.

AC Q43827; ID Q43827; DB 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)

OS CD76 (Angiopoietin-like factor) (CD76 protein).

GN Df647M16.1 OR CD76.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP [1]

SEQUENCE FROM N.A.

RA TISSUE=CORNEA;

RC Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Bagunley C.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RC TISSUE=SKIN;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21318995; PubMed=11426320;
 RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
 RA Vorup-Jensen T., Inel S., Friedl H., Hankeln T., Hall R., Gregory S.,
 RA Fujita T., Schwaeble W.;
 RT "The human gene for mannin-binding lectin-associated serine protease-2
 RT (MASP-2), the effector component of the lectin route of complement
 RT activation, is part of a tightly linked gene cluster on chromosome
 RT 1p36.2-3.";
 RL Genes Immun. 2:119-127(2001).
 DR EMBL; Y16133; CAA76078.1; -;
 DR EMBL; AL049653; CAB44734.1; -;
 DR EMBL; BC001881; AA01881.1; -;
 DR EMBL; AJ300188; CAC15571.1; -;
 DR HSP; P02671; IFZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 19.0%; Score 379.5; DB 4; Length 346;
 Best Local Similarity 29.1%; Pred. No. 2,7e-23;
 Matches 98; Conservative 57; Mismatches 123; Indels 59; Gaps 12;

QY 41 CEESCDVYKTKT-----REKKHMCNRLQNSIVSTRSTKILLRMMDEQASL 89
 DB 46 CEEKELAAQVANISLSISELNKQERDWSVVMQ--VMELESNKRMESERLTDAESKY 102
 QY 90 DYLSNOVVELMNNRVLLTTEVEFRKQLDPEFRRPVQSHGLDCTDIKD--TIGSVYKTPSG 146
 DB 103 SEMNQIDIMQLQAQVYVQTSADAI-----YDSSILYQKKYRISGYKKLPD 150
 QY 147 LYTHPREGSSYFEVNCMDMDYRGGWYVQKRIGIIDFORLWCDYLDGFSDLLGEFWLG 206
 DB 151 DFLGSP-----LTFVCDMETSGGGWTIIQRKSGLSVFDYDMKQYKQGFSGIRDFWLG 205
 QY 207 LKRTFYVQNKTSFMLVYALESEDDTLAYSYDNFMLEDTEFFKMLLGYSAG-DA 265
 DB 206 NEHHRISROPT--RLRVEDEWEGNLRVAYESHFVYGLNELNSYRLFGLGYTGAVGMDA 262
 QY 266 FRGLKEDNORAMPSTSDVNDGCRPACLVNGQSVKSCSHLNKKTGMFNECGLANLNG 325
 DB 263 LQ-----YHNNTAFSTFKDKNDNC-----LDKCAQL-RKGGVYVCCIDSDNLNG 305
 QY 326 IHFSGK--LLATGIQMGWTNRKNSPVKIKSVSKIR 360
 DB 306 VYRILGEHNKHLDGITWYGM--HGSTYSLKRVEMKIR 340

RESULT 9
 Q9D2D2
 ID Q9D2D2 PRELIMINARY; PRT; 496 AA.
 AC Q9D2D2;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DE 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
 DE enriched library, clone:5031400E18, full insert sequence (angiotensin
 DE 2).
 GN AGPT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi Y., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pezole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK019860; BAB31887.1; -;
 DR EMBL; BC027216; AAH27216.1; -;
 DR HSP; P02671; IFZD.
 DR MGD; MG1:1202890; Agpt2.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;

Query Match 19.0%; Score 379.5; DB 11; Length 496;
 Best Local Similarity 25.7%; Pred. No. 4.3e-23;
 Matches 111; Conservative 71; Mismatches 125; Indels 125; Gaps 16;

QY 3 VOGNVHSTSSVYNIYEDGSSNAKDESKNDYVCKEDCEESCDVYKTRTEKKHMCN 62
 DB 112 IQQNVVQNGT--AVMIEIGTSILNQTA-----QTRKLTDEAVQNGTRLEQL 160
 QY 63 LQNSIVSTRSTKILLRMMDEQASLDYLSNOVVELMNNRVLLTTEV----- 111
 DB 161 LQHSI-----STNKLKQILDO-----TSEINKLQNKNSFLQKVLDMGKHSQLO 207
 QY 112 -----RKQ--LDPEFRRPV-----QSHGLDCTDIKRTIGSVYR-- 142
 DB 208 SMKEQDELQVLYVSKQSSVIDELEKKTATATVNSLSLQKQH-----DLMETVNSLTTMM 262
 QY 143 -----TPSGLYTHPREGSSYFEVNCMDYRGGW 172
 DB 263 SSPNSKSSVALRKERQTFRCACELFKSGILTTSGLITLTPRNSTEIRKAYCDMDVGGGW 322
 QY 173 TVIQKRIGIIDFORLWCDYLDGFSDLLGEFWLGKRTFYVQNKTSFMLVYALESEDD 232
 DB 323 TVIQREDGSDVDFQRTWKEYKEGFGSPGGEYWLGNFEVSQLGQHR--YVLKIQDKMEG 380
 QY 233 TLAYASTYDNFMLEDTEFFKMLLGYSNAGDAFGLKEDNORAMPSTSDVNDGCRP 292
 DB 381 NEASHLYDHFLIAGEESYRHLTGLTGTAGKI-----SSISQPSDSDTSDSDNDKC-- 433
 QY 293 ACIVNGQSVKSCSHLNKKTGMFNECGLANLNGTTH-----ESGKLATGIQMGWTNRKNS 348
 DB 434 -----ICKSOMLS-GGMWFDACGPNLNGQITPOKQNTNKF--NGIKWTY--KGS 480
 QY 349 PVKIKSVSKIR 360
 DB 480 :|: :| :|

Db 481 GYSLKATMMIR 492

RESULT 10

Q9DER1 PRELIMINARY; PRT; 407 AA.

AC Q9DER1; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Angiopoietin-2B.

GN ANGIOPOIETIN-2B.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20422311; PubMed=10964717;

RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V., Vilagresa X., Mezquita C.,

RT "Genomic structure and alternative splicing of chicken angiopoietin-2."

RT Biochem. Biophys. Res. Commun. 275:643-651(2000).

RL EMBL; AJ289778; CAC08175.1; -.

DR HSSP; P02671; 1FZD.

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

SO SEQUENCE 407 AA; 46687 MW; 8863BA0AB8C7A1C CRC64;

Query Match 18.9%; Score 378.5; DB 13; Length 407;
Best Local Similarity 26.4%; Pred. No. 4e-23;
Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

QY 3 VGGNCVHSTDSVNVITVDGSAKDESKSNDYVCKEDDESDVTKTKITREKHKMCRN 62
DB 23 IQOTAAQNOT---AVMIEIGTMLNQT-----AEQTRKLDVAOYLNQTRLEQL 71
QY 63 LQNSIYSYRSTKRLKLR-----NMDEQOASLDYLSNOVNL----- 99
DB 72 LHSLS-----STNKLEROISVQTNELTKLOEKNSFLERKYLEKEDKHTLOLSIKDEKDO 126
QY 100 -----MNRVL-----LITTEVERKQDPPRRPVQS-HGL----- 128
DB 127 LGVLVARQNSIIELEKQLVATVNNSVLOKQOHDLMEVHNLMTISIPNSAKKNFIAR 186
QY 129 -----DCTD-IKDTIGSVTKPSGLYIIHPGSSYPFEVCMQMDYRGCGWTVIQKRID 180
DB 187 EQOISFKDCAEAFKSGL-----TTSGLTYLTFPPNSAQEKAKYCDMSNGGWTVALORRED 241
QY 181 GIIDFQRLACDYLDFGDDLGFEFGLGKIFVIYNOKNTSPMLYVLESDDTLAAASYD 240
DB 242 GSVDFHRTKKEKIKIGFDAGERYLGNESVQLTNOKR--YVAKITLKMEGNEATVLD 299
QY 241 NFWLEDETRFFKMHILGRYSGNAGDAFRLGKEDKNAMFESTSDVNDGCRPACLVNGOS 300
DB 300 QFYLANEEOQKYRIHLKGLGTAGKI-----SSISQPGNPFSTFADANDNC----- 344
QY 301 VASCSLHAKTKQWNEECGLANINGIH---FSGKLATGIQWGTWTKNNSPVKIKSYS 356
DB 345 ICKGSGMLT-GGWWFDACGSPNLNGMYPLRQNNKF--NGIKWYV--KSGSYSLKATV 399
QY 357 MKIR 360
DB 400 MMIR 403

RESULT 11

Q91589 PRELIMINARY; PRT; 488 AA.

AC Q91589; 091546;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Fibrinogen B-beta subunit precursor.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=93369693; PubMed=7642099;

RA Roberts L.R., Nichols L.A., Holland L.J.;

RT "cDNA and amino-acid sequences and organization of the gene encoding the B beta subunit of fibrinogen from Xenopus laevis.";

RT Gene 160:223-228(1995).

RL [2]

RP SEQUENCE OF 1-25 FROM N.A.

RX MEDLINE=94032285; PubMed=8218230;

RA Roberts L.R., Nichols L.A., Holland L.J.;

RT "Transcriptional regulation of the Xenopus laevis B beta fibrinogen subunit gene by glucocorticoids and hepatocyte nuclear factor 1: analysis by transfection into primary liver cells.";

RT Biochemistry 32:11627-11637(1993).

RL [3]

RP SEQUENCE OF 1-25 FROM N.A.

RA Holland L.J.;

RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; U19618; AAA85283.1; -.

DR EMBL; U05035; AAA60463.1; -.

DR HSSP; P02675; 1FZG.

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; fibrinogen_C; 1.

DR SMART; SM00186; FBG; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

KT Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 43 B FIBRINOPEPTIDE.

FT CHAIN 17 488 FIBRINOGEN B-BETA SUBUNIT.

SO SEQUENCE 488 AA; 54803 MW; 660E038444BC6414 CRC64;

Query Match 18.9%; Score 378.5; DB 13; Length 488;
Best Local Similarity 28.6%; Pred. No. 5.1e-23;
Matches 115; Conservative 49; Mismatches 143; Indels 95; Gaps 15;

QY 41 CEESCVYKTKITREKHF-----MCRNLQNSIVSTRSTKLLRMNMDQOASLDY 91
DB 106 CPTGCELRFTLLKQERNVKTAINDVGRVETLAQSANVRYRTYVLGQKIKENQOQTLDN 165
QY 92 LSNQVNL-----MNRVLITTEVERKQDPPRR----- 121
DB 166 -QNVVMEVNELEEQYTFKNDINDTIPKSNIRLROYLENLSKIQKLETAATOVENCR 224
QY 122 -----PVOSHGDCTDINDITGIVTKPSGLYIIHPGSSYPFEVCMQMDYRGCGM 172
DB 225 SPQVTCPIPVVS-GRECEIYRKGET-----SEMYLIQPDSEFRFRKYCCMATIDGWM 279
QY 173 TVYQKRIDGIIIDFQRLMCDYLDGFC-----DLGFEFGLGKIFVIYNOKNTSP 221
DB 280 TVYQNRQDSVSGRFTWDSYKSGFNIANGKGLCDMGFEFLGNEKISQLTNLGATPA 339
QY 222 MLYVALESDDTLAVASYNFMLEDRFRFKMHILGRYSGNAGDAFAG-----LKEDN----- 274
DB 340 LF--EMEDMDGAKVYAOYGTGYVQNEANKYQLSVSGYKGTAGALMDGASQLKGENRTMT 397
QY 275 -QNAPEFSTDVNDGCRPACLVNGOSVKSCHSHLHAKTKQWNEECGLANINGIHPSGKL 333
DB 398 IHNGMFEFTFDRNDGWMQ-----HSDPNKQCSK-EDGGGWVNYRCAANPNNGRYTYNGIY 451
QY 334 -----LATGIQWGTWTKNNSPVKIKSVSKIRMYNPF 367

DB 452 TWDMAKHGTDDGYVMNMW--KDSWYSMKKMSIKIR----PYF 487

RESULT 12
Q9DER2

PRELIMINARY: PRT: 493 AA.

AC Q9DER2; PRELIMINARY: PRT: 493 AA.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Angiopoietin-2A.
 GN ANGIOPOIETIN-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; PubMed=10964717;
 RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
 RA Villagrana X., Mezquita C.;
 RT "Genomic structure and alternative splicing of chicken angiopoietin-
 2".
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL; AJ289777; CAC08174.1; -.
 DR HSSP; P02671; 1F2D.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 493 AA; 56393 MW; BDIA21F90172F6DA CRC64;

Query Match 18.9%; Score 378.5; DB 13; Length 493;
 Best Local Similarity 26.4%; Pred. No. 5.2e-23;
 Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

QY 3 VQGNCHVHSTDSVYVNIEDGSAKDESKSNDTVCKEDCESCDVYKTRREEKHFCRN 62
 DB 109 IIOATAVQNGT---AVMIEIGTNLNGT-----ABQTRKLTVEVAQVLNGTRELQL 157
 QY 63 LQNSIVSYSTYKTLR-----NMDEQASLDYLSQVNEL----- 99
 DB 158 LEHSL-----STNKLEROISVQTEITRLOEKNSFLERVLKEMDKHTLQLSIKERDQ 212
 QY 100 -----MNRVL-----LTTEVFRKQLDPPHRYQS--HGL----- 128
 DB 213 LQYLVARQNSIIIELEKQVLTATVNSVLOKQOHDLMETVHNLMTSTPSAKNFIAK 272
 QY 129 -----DCTD-IKDTIGSVTKTPSGLYIHPGSSYPFEVMCDMDYRGGWTVIQRID 180
 DB 273 EEOISFMDCAEAFKSGI-----TSGIYTLTFPNSAQEKAYCDMESNGGWTVIQRRED 327
 QY 181 GIIDFOLKQDIDGFEFDLGEFYLGLKIFYIYNOKNTSPMLVVALESEDDTLATVSYD 240
 DB 328 GSVDFHTWKEIKYIGFDGPEGEYWLGNFVQSOLTKR--YVLTIIILKDWEGNEAYTLYD 385
 QY 241 NFWLEDETRFVKHMLGRYSNAGDAFRGLKEDNONAMPSTSDVDNDCGRPACTLVNGQS 300
 DB 386 QFYLANEEOYKRIHLKGLTGTAKI-----SSISQPGNDSTKADNDKC----- 430
 QY 301 VKSCSHLHNTGWMFNECGLANGLIH--FSGKLATGIOMGTWKNNSPYKIKSVS 356
 DB 431 ICKSQMLT-GGWWFDACGPNLNGMYTPLRQNNKF--NGIKWYV--KSGYSLKATY 485
 QY 357 MKIR 360
 DB 486 MKIR 489

RESULT 13
Q9DER0
PRELIMINARY: PRT: 441 AA.

AC Q9DER0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Angiopoietin-2C.
 GN ANGIOPOIETIN-2C.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; PubMed=10964717;
 RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
 RA Villagrana X., Mezquita C.;
 RT "Genomic structure and alternative splicing of chicken angiopoietin-
 2".
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL; AJ289779; CAC08176.1; -.
 DR HSSP; P02671; 1F2D.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 441 AA; 50472 MW; DC98127FEOCE34E2 CRC64;

Query Match 18.8%; Score 376.5; DB 13; Length 441;
 Best Local Similarity 30.3%; Pred. No. 6.6e-23;
 Matches 101; Conservative 61; Mismatches 122; Indels 49; Gaps 14;

QY 40 DCEESCVCVTKTRREEKH---FMCRLQNSIVSYTRS---TKLIRNMDEQASLDYL 92
 DB 142 EMEKHKLQLSIKDEKQDQVLVAR--QNSIIELEKQVLTATVNSVLOKQOHDL--- 196
 QY 93 SNOVNEIMNRVLLLTTEVFRKQLDPPHRYQSHGLDCTD-IKDTIGSVTKTPSGLYI 151
 DB 197 ---METVHNLMTSTPNSAK--NFAKEBOISFKCAEAFKSGI-----TSGIYTLT 246
 QY 152 PEGSSYFEVWCDMDYGGGWTVIQRIDGIIDFOLKQDIDGFEFDLGEFYLGLKIFY 211
 DB 247 FPNASOEKAYCDMESNGGWTVIQRREDGSDVDHRTWKEKIGFGDPAGEYWLGNFVS 306
 QY 212 YVYNOKNTSPMLVVALESEDDTLVASYDNFWLEDETRFVKHMLGRYSNAGDAFRGLK 271
 DB 307 QLTNQR--YVLTIIILKDWEGNEAYTLYDQYLANEEOYKRIHLKGLTGTAKI-----S 359
 QY 272 EDNONAMPSTSDVDNDCGRPACTLVNGQSVKSGHLLNKTGWMFNECGLANGLIH-- 328
 DB 360 SISQPGNDFSTKADNDKC-----ICKSQMLT-GGWWFDACGPNLNGMYTPLR 408
 QY 329 -FSGKLATGIOMGTWKNNSPYKIKSVKIR 360
 DB 409 QNNKF--NGIKWYV--KSGYSLKATYMKIR 437

RESULT 14
Q9D8W6
PRELIMINARY: PRT: 308 AA.
 AC Q9D8W6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Tachyplectin-5B isoform.
 OS Tachypleus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachypleus.
 NCBI_TaxID=6853;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99398666; PubMed=10468566;
 RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
 Mizuno Y., Wai S.N., Iwanaga S.,

QY 110 -----VERKQ-----LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEBEOCLRFHSQDTHVSPPLVQVYPQHHPNSQOYTPGLGNETIQRDGPYR 247
QY 129 DCTDIKDTIGSVTKTP-----SGLYIIHPGSSYPFEV 161
DB 248 DMPPLDLATSPKSPFKIPRYTFINEGPFKDCQOAKKAGHSVSGLYMKPKPENSNGPML 307
QY 162 MCDMDYRGCGMTVIOKRIIDGIDFQRLMCDYLDGFDGLGFEWLGKTFYVNOKNTSF 221
DB 308 KCENSIDPBGMTVIOKRIIDGIDFQRLMCDYLDGFDGLGFEWLGKTFYVNOKNTSF 365
QY 222 MLYVALESDPTLAAASYDNFWLEDETRPFKMHILGRYSGNADAFGLKEDNONAMPFS 281
DB 366 KLIIEEDMSDKKYAEYSFRLPESEFYRLRLGTGQNMADSMW-----HNGKQFT 419
QY 282 TSDVNDGCRPACLVNGOSVSKSHLHNTGWMFNECGLANLNGIHHSKTLA---TGI 338
DB 420 TLDROKD-----MYAGNCAHFH--KGMWYNACAHSNLNGWYRGHYSKHKODGI 468
QY 339 OMGTWTKNNSPYKIKSVSKIR 360
DB 469 FWAEX--RGGSYSLRAVOMIK 488

RESULT 2

US-08-960-507-4
; Sequence 4, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-960-507-4

Query Match 21.2%; Score 425; DB 3; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKESKSNIDVCKEDECSDVTKITRE-EKHFMCRNLONSIVSTRSTKILLRMM 82
DB 68 TKGDASTIKDITMDLENLKDVLISROKREIDVQLVVDGNIIVNEVKKILRKESRNM 127

QY 83 DE-QQASLDYL-----SNQVNEIMRVLTLTE----- 109
DB 128 SRVTOLYMOLHEILIRKRDNSLELSOLENKLIVTTEMLKATRYRELEVKYASLTDLVN 187
QY 110 -----VERKQ-----LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEBEOCLRFHSQDTHVSPPLVQVYPQHHPNSQOYTPGLGNETIQRDGPYR 247
QY 129 DCTDIKDTIGSVTKTP-----SGLYIIHPGSSYPFEV 161
DB 248 DMPPLDLATSPKSPFKIPRYTFINEGPFKDCQOAKKAGHSVSGLYMKPKPENSNGPML 307
QY 162 MCDMDYRGCGMTVIOKRIIDGIDFQRLMCDYLDGFDGLGFEWLGKTFYVNOKNTSF 221
DB 308 KCENSIDPBGMTVIOKRIIDGIDFQRLMCDYLDGFDGLGFEWLGKTFYVNOKNTSF 365
QY 222 MLYVALESDPTLAAASYDNFWLEDETRPFKMHILGRYSGNADAFGLKEDNONAMPFS 281
DB 366 KLIIEEDMSDKKYAEYSFRLPESEFYRLRLGTGQNMADSMW-----HNGKQFT 419
QY 282 TSDVNDGCRPACLVNGOSVSKSHLHNTGWMFNECGLANLNGIHHSKTLA---TGI 338
DB 420 TLDROKD-----MYAGNCAHFH--KGMWYNACAHSNLNGWYRGHYSKHKODGI 468
QY 339 OMGTWTKNNSPYKIKSVSKIR 360
DB 469 FWAEX--RGGSYSLRAVOMIK 488

RESULT 3

US-09-136-828-4
; Sequence 4, Application US/09136828
; Patent No. 6350450
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,828
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130R1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-136-828-4

Query Match 21.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKESKSNIDVCKEDECSDVTKITRE-EKHFMCRNLONSIVSTRSTKILLRMM 82

Db 68 TKGDASTIKDMITRMDELKDVLSRKREIDVLOLVVDGNIVNEVLLRKESHNM 127
QY 83 DE-QQASLDYL-----SNQVNEIMNRVLLTTE----- 109
Db 128 SRVQLYMQLLHETIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
Db 188 NQSVMITLLEECRLRIFSRQDTHVSPPLVQVPHIPNSQOQYTPGLLGNEIQDPGYP 247
QY 129 DCTDIDKDTIGSVTKTP-----SGLYIHPGSSYPFEV 161
Db 248 DLMPPPLATSPKSPKIPPVTFINEGPDKCOQAKKASHSVSGIYMIKRPENSGPMOL 307
QY 162 MCDMDYRGSGMTYQKRIIDIFQRLMCDYLDGFDLGEFNLGKIKIFYIYNQKTSF 221
Db 308 WCENSIDPGMTYQKRTDSSVNFERNMENTKGFNIDETWGLNITMLSNQDN--Y 365
QY 222 MLYVALESEDDTLAYASYDNFMLEDETFRFKMLGRYSGNAGDAFRGLKEDNONAMPFS 281
Db 366 KLIELEDMDKRYAYEYSFRLPESEFYRLRGTYQGNAGDSMM-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGQSVKCSHLNKTGWFNEBGLANLNGIHFSKLLA---TGT 338
Db 420 TLDRDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
QY 339 QMGWTKNNSPVKIKSVSMKIR 360
Db 469 FMAEY--RGGSYSLRAVQMMIK 488

RESULT 4
US-09-332-928A-4

; Sequence 4, Application US/09332928A
; Patent No. 6368853

; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.

; Gurney, Austin L.

; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,928A

; FILING DATE: 14-Jun-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.

; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-332-928A-4
Query Match 21.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKDESKNDYCKEDCESCDVKTKITRE-EKHEFCRMLQNSIYSTSTKLLRNM 82
Db 68 TKGDASTIKDMITRMDELKDVLSRKREIDVLOLVVDGNIVNEVLLRKESHNM 127
QY 83 DE-QQASLDYL-----SNQVNEIMNRVLLTTE----- 109
Db 128 SRVQLYMQLLHETIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
Db 188 NQSVMITLLEECRLRIFSRQDTHVSPPLVQVPHIPNSQOQYTPGLLGNEIQDPGYP 247
QY 129 DCTDIDKDTIGSVTKTP-----SGLYIHPGSSYPFEV 161
Db 248 DLMPPPLATSPKSPKIPPVTFINEGPDKCOQAKKASHSVSGIYMIKRPENSGPMOL 307
QY 162 MCDMDYRGSGMTYQKRIIDIFQRLMCDYLDGFDLGEFNLGKIKIFYIYNQKTSF 221
Db 308 WCENSIDPGMTYQKRTDSSVNFERNMENTKGFNIDETWGLNITMLSNQDN--Y 365
QY 222 MLYVALESEDDTLAYASYDNFMLEDETFRFKMLGRYSGNAGDAFRGLKEDNONAMPFS 281
Db 366 KLIELEDMDKRYAYEYSFRLPESEFYRLRGTYQGNAGDSMM-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGQSVKCSHLNKTGWFNEBGLANLNGIHFSKLLA---TGT 338
Db 420 TLDRDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
QY 339 QMGWTKNNSPVKIKSVSMKIR 360
Db 469 FMAEY--RGGSYSLRAVQMMIK 488

RESULT 5
US-09-136-801-4

; Sequence 4, Application US/09136801
; Patent No. 6413770.

; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth

; APPLICANT: Botstein, David

; APPLICANT: Goddard, Audrey

; APPLICANT: Roy, Margaret

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Tumas, Daniel

; APPLICANT: Schwall, Ralph

; TITLE OF INVENTION: Tie Ligand Homologues

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,801

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.

```

? REGISTRATION NUMBER: 33_055
? REFERENCE/DOCKET NUMBER: P113022
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-3216
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 4:
? SOURCE CHARACTERISTICS:
? LENGTH: 491 amino acids
? type: amino acid
? TOPOLOGY: Linear
US-09-136-801-4
```

Query Match	21.2%	Score 425	DB 4	Length 491
Best Local Similarity	26.9%	Pred. No. 3.2e-37		
Matches 119, Conservative	64	Mismatches 133,	Indels 126,	Gaps 14

QY	24	SNADSESNNTVCKEEDCEECQDVKTITRE--EKHFNCRNLONSIVSYSTSKLLNNM	82
Db	68	TKGDASTIKMTIRMDLENKVDLSQKREIDVQLVYDVGNIVAEVYLLKRESNNM	127
QY	83	DE-QQASLDYL-----SNQVNEIMNRVLLTTE-----	109
Db	128	SRVQLYMQLLHETIRKRDNSLELSQENKILNVTTEMLKATRYRELEVYASLTDLVN	187
QY	110	-----VRRKQ---LDP-----FHRVQSHGL-----	128
Db	188	NOSVMTLLLEEOLRIFSRODTHVSPLYOVVPHDNIENSQOYTPGLLGNEIORDPYR	247
QY	129	DCTDIKDTIGSVTKTP-----SGLYIHPEGSSPYEEV	161
Db	248	DLMPRLPLAITSPTSPKRIIPVYTFINSGPRCDQQAKEACHSVSGIYMITRPNSSNGPMQL	307
QY	162	MCDMDYRGGGATVIOKRIDIGTIDFORLWCDYLDGFGDLGEFWLGLKRIEYIVQNKTSF	221
Db	308	WCENSELDPGGCTVIOAKRTDSSVNFERNMEYWKKGFCGNDIEYWLGTENIYMLSNOD--Y	365
QY	222	MLYVALESEDDTLAVASYADNFWLEDETRFRKMHGRSGNAGCAFRLEKREDONAMPES	281
Db	366	KLIIIELEDWSDKKYAYAESFRLEPESEEFRLRLGTYQGNAGDSMMH-----HNGKQFT	419
QY	282	TSDVDNDGCRPACLVNGQSVKSCSHLNLNKGWFMNECGLLNGLNGIHHSCKLLA--TGI	338
Db	420	TLDRDKD-----MYAGNCNHFH-KGGWMTNACAHSLNGLNGVYVRGGHHYSKHQDGI	468
QY	339	QMGWTYTKNNSPVKIKSVSMKIR	360
Db	469	FWAEY--RGGSYSILRAVOVMIK	488

RESULT 6
US-09-332-929-4
Sequence 4, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:

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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/933,821
4
5 FILING DATE:
6
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Dregler, Glaser R.
9 REGISTRATION NUMBER: 33,055
10 REFERENCE/DOCKET NUMBER: P11300
11
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 650/225-5216
14
15 TELEFAX: 650/952-9881
16
17 INFORMATION FOR SEQ ID NO: 4:
18
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 491 amino acids
21 TYPE: Amino Acid
22 TOPOLOGY: Linear
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Query Match	21.2%	Score 425	DB 4	Length 491
Best Local Similarity	26.9%	Pred. No.	3.2e-37	
Matches 119	Conservative 64	Mismatches 133	Indels 126	Gaps 14

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QY 24 SNADESKSNDYVCKEDECESCDVKTITRE--EKHFRCRNLONSIVTSTFKLLBNMM 82
Db 68 TKGDASTIKDMITRMLDENIKDVL$KQKREIDVLVDYDGNIVAEVKLLRESRNMN 127
QY 83 DE-QQASLDYL-----SNOVNEIMNRVLLTTE----- 109
Db 128 SRVQLYMWQLHEIIRKRDNSLELSQENKILANTTEMKMA7RYRELEVKASLVDLVN 167
QY 110 -----VRRKQ---LDP-----FHRPVQSHGL----- 128
Db 188 NOSVMTLLEEQCLIRFSKODTHVSPRLVQVVRPHIENS00VYTPGGLGNEIORDPYR 247
QY 129 DCDTIDKDTIGSVTTP-----SGLYIHPEGSSYFEEV 161
Db 248 DLMPPRLATSPKSPKIRPVYTFINEGPRFKDQQAKEAGHSVSGIYMIKPNNSGMQL 307
QY 162 MCDMDYRGCGWTVYOKRIDGILDFORLWCDYLDGFGLLDCEFWLGLKFIYVQKNTSF 221
Db 308 WCENSLDPGGVTVYOKRTDGSVNFENFRMWEYMKKQFGNIDEWYGLGENIYML$NODN--Y 365
QY 222 MLYVALESEDDTLLAYSYDNPWLEDETRFPMHILGR$VGNAGDAFRLEKKEDONAMPFS 261
Db 366 KLILIELEDMSKKKAYAEYSFRLEPESEF7RLRLGITYQ$NAGDSMMV-----HNGKQFT 419
QY 282 TSDVDNDGCRPACILVNGQSVKSCGSHLANKTGWMEFNEGGLNIIHFSKLLA--TGI 338
Db 420 TLDRDKD-----MYAGNC$HNF-KGGMWYNAC$HNSLNGVNYRGHYSKHDGI 468
QY 339 QMGWTVTKNNSPVKIKSY$MIR 360
Db 469 FWAEEY--RGGSYSLR$AVOMMK 488

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RESULT 7 -133A-2
US-09-442-143A-2
: Sequence 2, Application US/09442143A
: Patent No. 6403089
: GENERAL INFORMATION:
: APPLICANT: Levy, Gary
: APPLICANT: Clark, David A.
: TITLE OF INVENTION: Methods of Modulating Immune Coagulation
: FILE REFERENCE: 9579-14
: CURRENT APPLICATION NUMBER: US/09/442,143A
: CURRENT FILING DATE: 1999-11-15
: PRIOR APPLICATION NUMBER: US 60/046,537
: PRIOR FILING DATE: 1997-05-17
: PRIOR APPLICATION NUMBER: US 60/061,684
: PRIOR FILING DATE: 1997-10-10
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2

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OY 63 LONSIYSY-----TRSTFKLLRNMM 82
|:|:|:|:|
DB 157 LENSISTYLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEKENLQGLV 216
|:|:|:|:|
OY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLTTEVF-----RKOLDPPP 119
|:|:|:|:|
DB 217 TRQTYIIQLEKQLNATTNNSVLOKQOLEMDTVNHLVNLCTKEVLLGCKREEKPP- 275
|:|:|:|:|
OY 120 HRPVOSHGLDCTDIKDTISVTKTPSGLYIIHPEGSSYFEVWCDMDYGGCTVYQKRI 179
|:|:|:|:|
DB 276 -----RDCADVY-----QAGFNKSGITYIYINNPEPKKVCNNDVNGGCTVYQHRE 323
|:|:|:|:|
OY 180 DGLIDFQRLMCDYLDGFGDLLEFWMGLKFIYVNOCKNTSPFLVYALSEDDDTLAYASY 239
|:|:|:|:|
DB 324 DGSLDQKQKKEKMGFGNPSGEYWLGNFPAITSQR--QVLRLELMDWEGNRAYSQY 381
|:|:|:|:|
OY 240 DNFWEDETRFRKMLGRYSGNAGDAFRGLKKEDN--QNAPEFSTSDVNDGCRPAC--L 295
|:|:|:|:|
DB 382 DRFHIGNEKQNRRLYLKGTGTAG-----KQSLILHGADEPSTKDAUDNDCMKCALM 434
|:|:|:|:|
OY 296 VNGOSYKSCSHLHNTGWMFNECGLANLNGIHFS-----GKLLATIGQGTWTKNNSPVK 351
|:|:|:|:|
DB 435 LFG-----GWMFADAGPSNLNGMFTYTAGQNHGKL--NGIKWHYF--KGPSYS 477
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OY 352 IKSVMKIR 360
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DB 478 IRSTTMIR 486
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RESULT 10
US-09-709-188-12
; Sequence 12, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular InterCellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; PRIORITY FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIORITY FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-12
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Query Match 20.3%; Score 405.5; DB 4; Length 490;
Best Local Similarity 27.5%; Pred. No. 4,1e-35;
Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

OY 3 VQNCYHNSSTDSSVNIIVEDGSNAKDESKSNDTVCKEDCESCDYKTKITREKHPMCRN 62
|:|:|:|:|
DB 108 IOONAVQNHNT-----ATMLEIGTSLSQT-----AEQTRKLTVDVETQVLANQTSRLQIDL 156
|:|:|:|:|
OY 63 LONSIYSY-----TRSTFKLLRNMM 82
|:|:|:|:|
DB 157 LENSISTYLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEKENLQGLV 216
|:|:|:|:|
OY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLTTEVF-----RKOLDPPP 119
|:|:|:|:|
DB 217 TRQTYIIQLEKQLNATTNNSVLOKQOLEMDTVNHLVNLCTKEVLLGCKREEKPP- 275
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OY 120 HRPVOSHGLDCTDIKDTISVTKTPSGLYIIHPEGSSYFEVWCDMDYGGCTVYQKRI 179
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DB 276 -----RDCADVY-----QAGFNKSGITYIYINNPEPKKVCNNDVNGGCTVYQHRE 323
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OY 180 DGLIDFQRLMCDYLDGFGDLLEFWMGLKFIYVNOCKNTSPFLVYALSEDDDTLAYASY 239
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DB 324 DGSLDQKQKKEKMGFGNPSGEYWLGNFPAITSQR--QVLRLELMDWEGNRAYSQY 381
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OY 240 DNFWEDETRFRKMLGRYSGNAGDAFRGLKKEDN--QNAPEFSTSDVNDGCRPAC--L 295
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DB 382 DRFHIGNEKQNRRLYLKGTGTAG-----KQSLILHGADEPSTKDAUDNDCMKCALM 434
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OY 296 VNGOSYKSCSHLHNTGWMFNECGLANLNGIHFS-----GKLLATIGQGTWTKNNSPVK 351
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DB 435 LFG-----GWMFADAGPSNLNGMFTYTAGQNHGKL--NGIKWHYF--KGPSYS 477
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OY 352 IKSVMKIR 360
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DB 478 IRSTTMIR 486
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RESULT 11
US-08-740-223A-4
; Sequence 4, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; NUMBER OF SEQUENCES: 28
; TITLE OF INVENTION: InterCellular Signalling Molecule
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Covert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; FEATURE:
; NAME/KEY: Human TIE-2 ligand 1
; LOCATION: 1...216
; OTHER INFORMATION: from T986 clone
US-08-740-223A-4
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Query Match 20.2%; Score 403.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No. 6,9e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 3 VQNCYHNSSTDSSVNIIVEDGSNAKDESKSNDTVCKEDCESCDYKTKITREKHPMCRN 62
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DB 115 IOONAVQNHNT-----ATMLEIGTSLSQT-----AEQTRKLTVDVETQVLANQTSRLQIDL 163
|:|:|:|:|
OY 63 LONSIYSY-----TRSTFKLLRNMM 82
|:|:|:|:|
DB 164 LENSISTYLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEKENLQGLV 223
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OY      83 DEOASLDYLSNOVN-----ELM-----NRVLLTTEVE-----RKOLDPP 119
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Db      224 TRQTYIIIOLELKO.NRRATNTNSVLOKQOOLELMDTVNHLVLCREVLKCGKREEKPP- 282
        | : : | : |
OY      120 HRPVQSHGLDCTDIDKPTIGSVTKPSGLYIIIEHGSSSYPPEWCMDDMDRGCGVTYIOKRI 179
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      283 -----RCDADY-----QAGFMKSSIIYIIYINMEPEPKYVCNMDYNGGGTIVIOHRE 330
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      180 DGIIDFORLWCDYLDGFGDILGEEFMIKIKFYIVNOKNTSPMLUYALASEDDTLVAYSY 239
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Db      331 DGSIDFQRMKEYKMGKGNPSGEYWLGNEFIATISQ- QYMLRIELMDWENRAYSQY 368
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OY      240 DNFWELEDTREFKMHLCIRYSGNAGDAFGLKKEDN- QNAMPSTSDVDNDGCRPAC--L 295
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Db      389 DRFHNGENQWRYRLYLKGHTGTAG-----KOSLIIAGDSEFKDADNDNCMCALM 441
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RESULT 12
US-09-709-188-4
; Sequence ID#, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-709-188-4

Query Match          20.2%; Score 403.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No.6,9e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY      3  VQGNCVHHSTDSVVNIVEDGSAKDESKNDTYCKEDCESCDVKTKITREKHFMCRN 62
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Db      115 IQGNANVOHNT---ATMLEIGTISLSOT-----ABQTRKLIDVETQVLNQRSLEIQI 163

QY      63  LONSIIVSY-----TRSTKKLRNMK 82
       ||::||::||:
Db      164 LENSIISTYKLEKOLLQOOTNELTIHEKNSLIEHKILEMBESKHKEBELDTKEERENLOGLV 223

QY      83  DEQOASLDIYSNOVN-----EIM-----NRVLILTTEVF-----RKOLDPEP 119
       |::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      224 TRQFYIIIELEKOLNRATNTNNSVLQKOELLEMDPVHNLMVLCKREYLLKKGKREEKEPF 282

QY      120 HRPVOSHLDCTDIDKPTIGSVTKTPPSGLYIIHPGSSYPFEVWCAMDMDYRGCGMTVIQAKRI 179
        ||::||::||::||::||::||::||::||::||::||::||::||::||
Db      283 -----RDCADAVY----QAQFNKSGIITYIYINMDEPKRVPCNMDVNGGGTVIQHHR 330

QY      180 DGIIDFQRLMCDDYLDGFDLLGEFMLGIKIKIFYIVNOKNTSPMLUYALESEDPTLAYASY 239
       ||::||::||::||::||::||::||::||::||::||::||::||::||
Db      331 DGSLDFQRCWKMEYKMGFGNPBGCEYWLGNELFIATTSQR--QYMIRIELMWEGNRRAYSQY 388

QY      240 DNFWLEDETREFKMHLCGRYSGNAGDAFRGLKKEDN--QNAMPSTSDVDNDGCRPAC--L 295
       ||::||::||::||::||::||::||::||::||::||::||::||::||
Db      389 DRFLIGNEKNQYRYLGLGHGTAG-----KOSLIIGHGADSTSRKADNDNCMCACALM 441

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Oy 296 VNGSVKSCSHLHNKTGMWFNECGLANGTIHHSG-----KLATGIGOMTWTNNNSPVK 351
 :| | | | | | :| | | | | | :| | | | | |
Db 442 LMG-----GWFPDAGCSNLNCFYTAGOHRRL--NGIKWHYF--KGFSYS 484

Oy 352 IKSVSMKR 360
Db 485 LRSTTMIR 493

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:      RESULT 13
:      US-08-373-579-4
:      Sequence 4, Application US/08373579
:      Patent No. 5650490
:      GENERAL INFORMATION:
:      APPLICANT: Davis, et al.
:      TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
:      TITLE OF INVENTION: THEREOF
:      NUMBER OF SEQUENCES: 6
:      CORRESPONDENCE ADDRESS:
:      ADDRESSEE: Regeneron Pharmaceuticals, Inc.
:      STREET: 777 Old Saw Mill Road
:      CITY: Tarrytown
:      STATE: New York
:      COUNTRY: USA
:      ZIP: 10591
:      COMPUTER READABLE FORM:
:      MEDIUM TYPE: Floppy disk
:      COMPUTER: IBM PC compatible
:      OPERATING SYSTEM: PC-DOS/MS-DOS
:      SOFTWARE: Patentln Release #1.0, Version #1.30
:      CURRENT APPLICATION DATA:
:      APPLICATION NUMBER: US/08/373,579
:      FILING DATE: 17-JAN-1995
:      CLASSIFICATION: 435
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/353,503
:      FILING DATE: 09-DEC-1994
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/348,492
:      FILING DATE: 02-DEC-1994
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/330,261
:      FILING DATE: 27-OCT-1994
:      PRIOR APPLICATION DATA:
:      APPLICATION NUMBER: US 08/319,932
:      FILING DATE: 07-OCT-1994
:      ATTORNEY/AGENT INFORMATION:
:      NAME: Cobert, Robert J.
:      REGISTRATION NUMBER: 36,108
:      REFERENCE/DOCKET NUMBER: REG 330-D
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (914) 345-7400
:      TELEFAX: (914) 345-7721
:      INFORMATION FOR SEQ ID NO: 4:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 497 amino acids
:      TYPE: amino acid
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      US-08-373-579-4

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Query Match	20.1%	Score 402.5	DB 1	Length 497
Best Local Similarity	27.3%	Pred No. 8	9e-35	
Matches	117	Conservative	66	Mismatches 125, Indels 121, Gaps 16
OY	3	VQGNQVHSTDSVYNIYEDGSGNADSEKSNIDTVCKEDCEESDYKTKITREKHFMCN	62	
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	:	:	:	:
DB	115	IQQNNVQNNH--ATMLEIGTSLSQT-----AEQRRKLTVDTQVLTQNSRLLEIQ	163	
OY	63	LQNSIVSY--		TRSTKRLLRNM 82
	:	:	:	:
DB	164	LENSITSTKLEKQLOQNEILIKIEKNSLLEKILLEMGEKHKREEDLTLEKEKENIQGVY	223	
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Db 248 DLMPPDLATSPYKSPFKIPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMOL 307
Qy 162 MCDMDYRGGGWTYQKRIDGIIIDFORLWCDYLDGREGDILGGEWLGKTKFYVYNQKNTSF 221
Db 308 WCENSLDPGGWTVQKRTDGSVNFRRMENVYKGFNGINDGEYWLGLNENTYMLSDNODN--Y 365
Qy 222 MLYVALESDDVDLAYASYDNFWLEDETRFVKMLHGRYSNAGDAFRGLKEKNONAMPSP 281
Db 366 KLIIELEMDSDKKYVAEYSSFRLEPESEFYRLRLGTIOGNADSDMMW-----HNGKQFT 419
Qy 282 TSDVDNDGCRPACLVNGSVKCSHLHNTGWMFNECGLANLNGIHFSGLKLA--TGI 338
Db 420 TLDROKD-----WYAGNCAPH--KGMWYNACANSLNNGVYRGHTRSKHODCI 468
Qy 339 OMGITWKNSPYKIKSVSKIR 360
Db 469 FWAEX--RGSYSRLAVOMMIK 488

RESULT 2
US-10-179-744-4
; Sequence 4, Application US/10179744
; Patent No. US20020173627A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10/179,744
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US/08/817,318
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-10-179-744-4

Query Match 20.1%; Score 402.5; DB 9; Length 497;
Best Local Similarity 27.3%; Pred. No. 2,4e-30;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

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Qy 63 LQNSIVSY-----TRSTRKLLRNMM 82
Db 164 LENSISTYKLEKQILOQTNELIKIHEKNSLLEHKLLEMEGKHKEELDTLKEKENIQGLV 223
Qy 83 DEQOASLDYLSNQVN-----ELM-----NRVLTLTTEYF-----RKOLDPPR 119
Db 224 TRQYTIIELEQLKRAATNNNSVLOKQOLEMDYVHNVLNCTKEYLLKGGKREEKRP- 282
Qy 120 HRPVOSHGLDCTDIDKTIGSVTKRPSGLYIHPRESSYRFEVYMDMDYRGGGWTVYQKRI 179
Db 283 -----RDCADYV-----QAGFNKSGIYTYIINNPEPKYFCNMNDVYGGGWTVYQHRE 330
Qy 180 DGIIDFORLWCDYLDGFGDILGEFWLGLKTKFYVYNQKNTSMLYVALESEDITLAYASY 239
Db 331 DGSLDFOGKWEYKMGFGSPGSEYWLGNFEIFAITSQR--QYMLRIELMDWEGNRAYSQY 388
Qy 240 DNFWLEDETREFKMLHGRYSNAGDAFRGLKEDN--ONAMFSTSDVYNDGCRPAC--L 295
Db 389 DRFHIGNEKQVNRILYKLGHTGTAG-----KQSSILLHGADFSTRKADNDNCKCKCALM 441
Qy 296 VNGSVKSCSHLHNTGWMFNECGLANLNGIHFS---GKLLATGIGOWGTTKNNSPYK 351
Db 442 LTG-----GMMFIDACGPSNLGMFTYAGQNNKGL--NGIKNHYE--KGPSYS 484

Qy 352 IKSVMKIR 360
Db 485 LRSTYMIIR 493
RESULT 3
US-10-066-500-4
; Sequence 4, Application US/10066500
; Patent No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gottlsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130RIC7
; CURRENT APPLICATION NUMBER: US/10/066,500
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1997-12-16
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; PRIOR FILING DATE: 1998-02-09
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; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/081049

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2	PRIOR APPLICATION NUMBER:	60/095998
3	PRIOR FILING DATE:	1996-08-10
4	PRIOR APPLICATION NUMBER:	60/097000
5	PRIOR FILING DATE:	1996-08-18
6	PRIOR APPLICATION NUMBER:	60/099601
7	PRIOR FILING DATE:	1996-09-09
8	PRIOR APPLICATION NUMBER:	60/099803
9	PRIOR FILING DATE:	1996-09-10
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15	PRIOR FILING DATE:	1996-09-17
16	PRIOR APPLICATION NUMBER:	60/101922
17	PRIOR FILING DATE:	1996-09-24
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19	PRIOR FILING DATE:	1996-10-28
20	PRIOR APPLICATION NUMBER:	60/109304
21	PRIOR FILING DATE:	1996-11-20
22	PRIOR APPLICATION NUMBER:	60/125778
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24	PRIOR APPLICATION NUMBER:	60/139695
25	PRIOR FILING DATE:	1999-06-15
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27	PRIOR FILING DATE:	1999-07-20
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36	PRIOR APPLICATION NUMBER:	08/933821
37	PRIOR FILING DATE:	1997-09-19
38	PRIOR APPLICATION NUMBER:	08/960507
39	PRIOR FILING DATE:	1997-10-29
40	PRIOR APPLICATION NUMBER:	09/114844
41	PRIOR FILING DATE:	1996-07-14
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43	PRIOR FILING DATE:	1996-08-19
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53	PRIOR FILING DATE:	1996-12-08
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61	PRIOR FILING DATE:	1999-04-15
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70	PRIOR APPLICATION NUMBER:	09/380137
71	PRIOR FILING DATE:	1999-08-25
72	PRIOR APPLICATION NUMBER:	09/380138
73	PRIOR FILING DATE:	1999-08-25

1	PRIOR APPLICATION NUMBER: 09/380139
2	PRIOR FILING DATE: 1999-08-25
3	PRIOR APPLICATION NUMBER: 09/403296
4	PRIOR FILING DATE: 1999-10-18
5	PRIOR APPLICATION NUMBER: 09/403297
6	PRIOR FILING DATE: 1999-10-18
7	PRIOR APPLICATION NUMBER: 09/423741
8	PRIOR FILING DATE: 1999-11-10
9	PRIOR APPLICATION NUMBER: 05/423844
10	PRIOR FILING DATE: 1999-11-12
11	PRIOR APPLICATION NUMBER: 09/522342
12	PRIOR FILING DATE: 2000-03-09
13	PRIOR APPLICATION NUMBER: 09/548815
14	PRIOR FILING DATE: 2000-04-13
15	PRIOR APPLICATION NUMBER: 09/664610
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17	PRIOR APPLICATION NUMBER: 09/665350
18	PRIOR FILING DATE: 2000-09-18
19	PRIOR APPLICATION NUMBER: 09/709238
20	PRIOR FILING DATE: 2000-11-08
21	PRIOR APPLICATION NUMBER: 09/767609
22	PRIOR FILING DATE: 2001-01-22
23	PRIOR APPLICATION NUMBER: 09/802706
24	PRIOR FILING DATE: 2001-03-09
25	PRIOR APPLICATION NUMBER: 09/808689
26	PRIOR FILING DATE: 2001-03-14
27	PRIOR APPLICATION NUMBER: 09/866028
28	PRIOR FILING DATE: 2001-05-25
29	PRIOR APPLICATION NUMBER: 09/870574
30	PRIOR FILING DATE: 2001-05-30
31	PRIOR APPLICATION NUMBER: 09/872035
32	PRIOR FILING DATE: 2001-06-01
33	PRIOR APPLICATION NUMBER: 09/886342
34	PRIOR FILING DATE: 2001-06-19
35	PRIOR APPLICATION NUMBER: 09/US98/14552
36	PRIOR FILING DATE: 1998-07-14
37	PRIOR APPLICATION NUMBER: PCT/US98/18824
38	PRIOR FILING DATE: 1998-09-10
39	PRIOR APPLICATION NUMBER: PCT/US98/190933
40	PRIOR FILING DATE: 1998-09-14
41	PRIOR APPLICATION NUMBER: PCT/US98/19330
42	PRIOR FILING DATE: 1998-09-16
43	PRIOR APPLICATION NUMBER: PCT/US98/19437
44	PRIOR FILING DATE: 1998-09-17
45	PRIOR APPLICATION NUMBER: PCT/US98/24855
46	PRIOR FILING DATE: 1998-11-20
47	PRIOR APPLICATION NUMBER: PCT/US98/25108
48	PRIOR FILING DATE: 1998-12-01
49	PRIOR APPLICATION NUMBER: PCT/US98/25190
50	PRIOR FILING DATE: 1998-11-25
51	PRIOR APPLICATION NUMBER: PCT/US99/050288
52	PRIOR FILING DATE: 1999-03-08
53	PRIOR APPLICATION NUMBER: PCT/US99/12252
54	PRIOR FILING DATE: 1999-06-02
55	PRIOR APPLICATION NUMBER: PCT/US99/20111
56	PRIOR FILING DATE: 1999-09-01
57	PRIOR APPLICATION NUMBER: PCT/US99/205944
58	PRIOR FILING DATE: 1999-09-08
59	PRIOR APPLICATION NUMBER: PCT/US99/210950
60	PRIOR FILING DATE: 1999-09-15
61	PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match	20.0%;	Score 400;	DB 9;	Length 493;
Best Local Similarity	31.9%;	Pred. No. 4.1e-30;		
Matches 94;	Conservative 50;	Mismatches 93;	Indels 58;	Gaps 11

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QY 63 LONSIYSY-----TRSTKLLNNM 82
  164 LENSISTYKLEKOLLQOTNEILKHEKNSLLEHKILEMEGKHKELDTLKEKENLOGLV 223
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  224 TRQTYIIQOELEKOLNRTATNNSVLQKQOELMDTVHNLVNLCTKEGVLLKGGKREEKPF 283
QY 119 PHRPVOSHGLDCTDIKDTIGSVTKTPSGLYIIPREGSSYPFEVWCDMDYGGGWTYIOKR 178
  284 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCNMDVGGGWTYIOHR 330
QY 179 IDGIIDFQRLMCDYLDGFGDLGFEWLGKFIYIVNQKNTSEMLYVALESEDOTLAYAS 238
  331 EDGSLDFQRGWKYKMGFGNPSGEYWLGNFEIFAITSQR--QYMLRIELMDWEGNRAYSQ 388
QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QANMPSTSDVNDGCRPAC-- 294
  389 YDRFHIGNEKQNRRLYLKGTGTAG-----KQSSLLHGADEFSTDADNDNCMCAL 441
QY 295 LVNGQSVKSCSHLNKGTWMPNECGLANLINGIHFS-----GKLLATGIOMGTWTKNNSPV 350
  442 MLTG-----GWMFDACGSPSNLNGMFTYTAQONHCKL--NQIKMHYF--KGPSY 484
QY 351 KIKSVSMKIR 360
  485 SLRSTTMMIR 494

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RESULT 7

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US-09-897-306-13
; Sequence 13, Application US/09897306
; Patent No. US20020123054A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Patterson, Chandra
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN ANGIOPOIETIN
; FILE REFERENCE: PC-0048 CIP
; CURRENT APPLICATION NUMBER: US/09/897,306
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020123054A1 g1907327
US-09-897-306-13

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Query Match 19.8%; Score 395; DB 10; Length 498;
 Best Local Similarity 27.0%; Pred. No. 1,2e-29;
 Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

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QY 63 LONSIYSY-----TRSTKLLNNM 82
  164 LENSISTYKLEKOLLQOTNEILKHEKNSLLEHKILEMEGKHKELDTLKEKENLOGLV 223
QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEF-----RKOLDPF 118
  224 TRQTYIIQOELEKOLNRTATNNSVLQKQOELMDTVHNLVNLCTKEGVLLKGGKREEKPF 283
QY 119 PHRPVOSHGLDCTDIKDTIGSVTKTPSGLYIIPREGSSYPFEVWCDMDYGGGWTYIOKR 178
  284 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCNMDVGGGWTYIOHR 330

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QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QANMPSTSDVNDGCRPAC-- 294
  389 YDRFHIGNEKQNRRLYLKGTGTAG-----KQSSLLHGADEFSTDADNDNCMCAL 441
QY 295 LVNGQSVKSCSHLNKGTWMPNECGLANLINGIHFS-----GKLLATGIOMGTWTKNNSPV 350
  442 MLTG-----GWMFDACGSPSNLNGMFTYTAQONHCKL--NQIKMHYF--KGPSY 484
QY 351 KIKSVSMKIR 360
  485 SLRSTTMMIR 494

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RESULT 8

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US-09-998-831-5
; Sequence 5, Application US/09998831
; Patent No. US20020119153A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brecken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998,831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-831-5

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Query Match 19.7%; Score 394; DB 10; Length 495;
 Best Local Similarity 27.0%; Pred. No. 1,5e-29;
 Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

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  161 LENSISTYKLEKOLLQOTNEILKHEKNSLLEHKILEMEGKHKELDTLKEKENLOGLV 220
QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEF-----RKOLDPF 118
  221 TRQTYIIQOELEKOLNRTATNNSVLQKQOELMDTVHNLVNLCTKEGVLLKGGKREEKPF 280
QY 119 PHRPVOSHGLDCTDIKDTIGSVTKTPSGLYIIPREGSSYPFEVWCDMDYGGGWTYIOKR 178
  281 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCNMDVGGGWTYIOHR 327
QY 179 IDGIIDFQRLMCDYLDGFGDLGFEWLGKFIYIVNQKNTSEMLYVALESEDOTLAYAS 238
  328 EDGSLDFQRGWKYKMGFGNPSGEYWLGNFEIFAITSQR--QYMLRIELMDWEGNRAYSQ 385
QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QANMPSTSDVNDGCRPAC-- 294
  386 YDRFHIGNEKQNRRLYLKGTGTAG-----KQSSLLHGADEFSTDADNDNCMCAL 438
QY 295 LVNGQSVKSCSHLNKGTWMPNECGLANLINGIHFS-----GKLLATGIOMGTWTKNNSPV 350
  439 MLTG-----GWMFDACGSPSNLNGMFTYTAQONHCKL--NQIKMHYF--KGPSY 481
QY 351 KIKSVSMKIR 360
  485 SLRSTTMMIR 494

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Db 176 QOFLVYCEIDSGNGWIVFQKRILDSVDFKKNMIGYKKEGFHLSPTGTETFLNGNEKIHU 235
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Qy 324 NGIHHSFSGKL-----LATGIOMGTWTKNNSPVYKIKSVSMK 358
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RESULT 14
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; Sequence 1, Application US/09912741B
; Patent No. US20020131970A1
; GENERAL INFORMATION:
; APPLICANT: Allert, Dario C
; APPLICANT: Langulino, Lucia R
; APPLICANT: Thornton, George B
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
; TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
; FILE REFERENCE: 300,1D1V4
; CURRENT APPLICATION NUMBER: US/09/912,741B
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 09/347,877
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 08/748,150
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: US 08/232,532
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 08/139,562
; PRIOR FILING DATE: 1993-10-19
; PRIOR APPLICATION NUMBER: US 07/898,117
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: expressed
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: 88
; OTHER INFORMATION: site of glycosylation
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (153)...(182)
; OTHER INFORMATION: disulfide-bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (326)...(339)
; OTHER INFORMATION: disulfide-bond
US-09-912-741B-1
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Best Local Similarity 27.5%; Pred. No. 2e-26;
Matches 111; Conservative 52; Mismatches 138; Indels 102; Gaps 15;
Qy 32 SNDVCKED-----CESSCDV-----KTKITREKHFMCNRLNONSIVSTRSKILL 78
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Db 62 KAIQITVPDESSKPMIDATLKSRIIMEIIMKYEASILTFRDSSIRYLOEITVSNMOKI 121
Qy 104 LLTTEVFRKQLDPPRHP-----VQSH--GLDCTDIKDTISVTKTSGLTIHPSS 156

Db 122 VNIKEV--AOLEAQCQCECKDTVQIHDITGKDCD-----IANKKAKSGLFIIRPKRN 175
Qy 157 YPEPVNCDMDYKGGWTVIQRIDGIIDFORLMCDYLDGFDL---LGEFNLGLKKIFY 212
Db 176 QOFLVYCEIDSGNGWIVFQKRILDSVDFKKNMIGYKKEGFHLSPTGTETFLNGNEKIHU 235
Qy 213 IYNOKNTSFMLYALESEDDTLAYASYDNFWELEDFRFRKMLGRS -GNADAFRGLKK 271
Db 236 ISTQSAIPALRVELEDNMGRSTADYAMFKVGPEDAKYRLTYAYFAGDADAFDGFDF 295
Qy 272 ED-----NONAMFSTSDVNDGCRPACLYNGOSVYKSCSHLHKTKGMFNECGLANU 323
Db 296 GDDPSDKFTTSINGMCFSTWDNDNDKFEBCNCAEDGS-----GWMANKCHAGHL 344
Qy 324 NGIHHSFSGKL-----LATGIOMGTWTKNNSPVYKIKSVSMK 358
Db 345 NGVYYGGTYYSKASTPNGYDNGIINATW-----KTRWYSMK 380
RESULT 15
US-09-992-598-314
; Sequence 314, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

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64	PRIOR FILING DATE: 1998-07-02
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66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/091982

